


```

QY      61  ECGPALMKIKHVSNFVRKYSOTIAELQELQSPAKDPEVNSLYCGGHPAVOVYREKATG 120
DB      61  ECGPALMKIKHVSNFVRKYSOTIAELQELQSPAKDPEVNSLYCGGHPAVOVYREKATG 120
QY      121 DIAMKVMKKKALLAOBOVSFFEEERNIISRSTSPMIPQLOVAFODKNIHLYLMEBOVPG 180
DB      121 DIAMKVMKKKALLAOBOVSFFEEERNIISRSTSPMIPQLOVAFODKNIHLYLMEBOVPG 180
QY      121 DIAMKVMKKKALLAOBOVSFFEEERNIISRSTSPMIPQLOVAFODKNIHLYLMEBOVPG 180
DB      121 DIAMKVMKKKALLAOBOVSFFEEERNIISRSTSPMIPQLOVAFODKNIHLYLMEBOVPG 180
QY      181 DLISLNRVEDQDENILQFYLAELILAVHSVHLMGVHDIKPENILVDRTHIKLVDF 240
DB      181 DLISLNRVEDQDENILQFYLAELILAVHSVHLMGVHDIKPENILVDRTHIKLVDF 240
QY      241 GSAKAKNSNMVNAKPIGTPDYMAPEVLTVMNGDGCTGYGLDCDMMWSVCVITAYEMIYGR 300
DB      241 GSAKAKNSNMVNAKPIGTPDYMAPEVLTVMNGDGCTGYGLDCDMMWSVCVITAYEMIYGR 300
QY      301 SPPAEGTSARTFNNINMFORFLKFPDDPKVSDFLDIQSLCGQKERLKFEGLCCHPFF 360
DB      301 SPPAEGTSARTFNNINMFORFLKFPDDPKVSDFLDIQSLCGQKERLKFEGLCCHPFF 360
QY      361 SKIDMNNIRNSPPFPVPTLKSDDTSNFDSPKXNSWSSPCQLSPSGFSGEELPFVGFSS 420
DB      361 SKIDMNNIRNSPPFPVPTLKSDDTSNFDSPKXNSWSSPCQLSPSGFSGEELPFVGFSS 420
QY      421 YSKALGILGRSESVSGLSDPACTSSMEKKLLIKSKELQDSQCKHMEQEMTRLRHRS 480
DB      421 YSKALGILGRSESVSGLSDPACTSSMEKKLLIKSKELQDSQCKHMEQEMTRLRHRS 480
QY      421 YSKALGILGRSESVSGLSDPACTSSMEKKLLIKSKELQDSQCKHMEQEMTRLRHRS 480
DB      421 YSKALGILGRSESVSGLSDPACTSSMEKKLLIKSKELQDSQCKHMEQEMTRLRHRS 480
QY      481 EYBAVLSQKEVELKASFTORSLEODLATYITECSSLKRSLEOAPMEVSEDKALQOLH 540
DB      481 EYBAVLSQKEVELKASFTORSLEODLATYITECSSLKRSLEOAPMEVSEDKALQOLH 540
QY      541 DIREQSRKLOEIKEOEYOAQVEEMRLMMQLEBDLVASARRSDLYSELSRESLAAEFK 600
DB      541 DIREQSRKLOEIKEOEYOAQVEEMRLMMQLEBDLVASARRSDLYSELSRESLAAEFK 600
QY      601 RKATECOHKLKAKDQKPEVGYAKLEKINAEQOLKIOELQKLEKAVASTATELQ 660
DB      601 RKATECOHKLKAKDQKPEVGYAKLEKINAEQOLKIOELQKLEKAVASTATELQ 660
QY      649 ----AKERARELEKLONRDSESGIRKKLVEABEERHSLBNYVKLETTERENRLLKOD 704
DB      649 ----AKERARELEKLONRDSESGIRKKLVEABEERHSLBNYVKLETTERENRLLKOD 704
QY      705 IQTKSOQIQOMADKILELEEKHREAOVSAQHLVHLKQKQHYEBKIKVLNQIKKDLAD 764
DB      705 IQTKSOQIQOMADKILELEEKHREAOVSAQHLVHLKQKQHYEBKIKVLNQIKKDLAD 764
QY      765 KETLENNMQHREBAHEBKILISEOKAMITAMDSKIRSLFORIVEISEANKLAANSGLFT 824
DB      765 KETLENNMQHREBAHEBKILISEOKAMITAMDSKIRSLFORIVEISEANKLAANSGLFT 824
QY      825 QRMKKAQOEEMISLROOKFYLETQAGKLEAONRKLLEBQLEKISHOHSDNKRLLLETRL 884
DB      825 QRMKKAQOEEMISLROOKFYLETQAGKLEAONRKLLEBQLEKISHOHSDNKRLLLETRL 884
QY      841 QRMKKAQOEEMISLROOKFYLETQAGKLEAONRKLLEBQLEKISHOHSDNKRLLLETRL 900
DB      841 QRMKKAQOEEMISLROOKFYLETQAGKLEAONRKLLEBQLEKISHOHSDNKRLLLETRL 900
QY      885 REVLSLEHBEQKLELQKQTELQSLQERESQTLAQARAALSESOLROAKTELEETTAB 944
DB      885 REVLSLEHBEQKLELQKQTELQSLQERESQTLAQARAALSESOLROAKTELEETTAB 944
QY      901 REVLSLEHBEQKLELQKQTELQSLQERESQTLAQARAALSESOLROAKTELEETTAB 960
DB      901 REVLSLEHBEQKLELQKQTELQSLQERESQTLAQARAALSESOLROAKTELEETTAB 960
QY      945 EEBIQAALTARDEIORKFDALRNSCTVITDLEBQALQLTEDNANLNNQNYLSKQIDEAS 1004
DB      945 EEBIQAALTARDEIORKFDALRNSCTVITDLEBQALQLTEDNANLNNQNYLSKQIDEAS 1004
QY      961 EEBIQAALTARDEIORKFDALRNSCTVITDLEBQALQLTEDNANLNNQNYLSKQIDEAS 1020
DB      961 EEBIQAALTARDEIORKFDALRNSCTVITDLEBQALQLTEDNANLNNQNYLSKQIDEAS 1020
QY      1005 GAUDEIYQJSEYVDHPRREITERBMOQTSQKOTMEALKTTCTMLEBQVMDLALNDELIE 1064
DB      1005 GAUDEIYQJSEYVDHPRREITERBMOQTSQKOTMEALKTTCTMLEBQVMDLALNDELIE 1064
QY      1021 GAUDEIYQJSEYVDHPRREITERBMOQTSQKOTMEALKTTCTMLEBQVMDLALNDELIE 1080
DB      1021 GAUDEIYQJSEYVDHPRREITERBMOQTSQKOTMEALKTTCTMLEBQVMDLALNDELIE 1080
QY      1065 KERQWEMANSVLGDDEKSOFECEVRELQRMULDTEKQSRARADORTTESRQVVELAVENK 1124
DB      1065 KERQWEMANSVLGDDEKSOFECEVRELQRMULDTEKQSRARADORTTESRQVVELAVENK 1124
QY      1081 KERQWEMANSVLGDDEKSOFECEVRELQRMULDTEKQSRARADORTTESRQVVELAVENK 1140
DB      1081 KERQWEMANSVLGDDEKSOFECEVRELQRMULDTEKQSRARADORTTESRQVVELAVENK 1140

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QY      1125 BITALQOALKEOKLKAESLSDKLNDEKKHAMLENNASLQOKLETTERELKORLLEBOAK 1184
DB      1141 BITALQOALKEOKLKAESLSDKLNDEKKHAMLENNASLQOKLETTERELKORLLEBOAK 1200
QY      1185 LQOQMDLOQNHIFRLTOGLQOALDRADLKTERRSDLEYOLENIQVLYSHEKVMESTISQ 1244
DB      1201 LQOQMDLOQNHIFRLTOGLQOALDRADLKTERRSDLEYOLENIQVLYSHEKVMESTISQ 1260
QY      1245 QTKLIDFLQAKNDQPAKKKKGLFSRKEDPALPTQVPLQYNELKALAEKAKCABLEBA 1304
DB      1261 QTKLIDFLQAKNDQPAKKKKGLFSRKEDPALPTQVPLQYNELKALAEKAKCABLEBA 1305
QY      1305 LQKTRIELSARBEAARHAKTDHPSPATARQOAMSAIYRSPHOSAMSILAPSS 1364
DB      1306 LQKTRIELSARBEAARHAKTDHPSPATARQOAMSAIYRSPHOSAMSILAPSS 1365
QY      1365 RRKESSTPEEFSRRLKERMHNIPIHFVNGLMNRATKCAVCLDTVHFGHQAQSCLEQVM 1424
DB      1366 RRKESSTPEEFSRRLKERMHNIPIHFVNGLMNRATKCAVCLDTVHFGHQAQSCLEQVM 1425
QY      1425 CHPKSCCLPATCGLPABYATHTFAFCRDKNNSPOLQTKESPSSLHLEGMKVPPNNKR 1484
DB      1426 CHPKSCCLPATCGLPABYATHTFAFCRDKNNSPOLQTKESPSSLHLEGMKVPPNNKR 1485
QY      1485 GQGMGRKTYVLBGSVLLYDNEABEAGORPYEEPELCLPDGVSITHGAVGASELANAK 1544
DB      1486 GQGMGRKTYVLBGSVLLYDNEABEAGORPYEEPELCLPDGVSITHGAVGASELANAK 1545
QY      1545 A-----EKABADAKL 1554
DB      1546 ADVPYLKNESHPIHTTCWPGRTLYLLAPSPDKQKVTALBESVAGRVSRBEAEADAKL 1605
QY      1555 LGNSLILKEGDRDLDMNCTLPSPDOVVLVTEBGLYALNVLKNSLTHVPGIGAVQIYII 1614
DB      1606 LGNSLILKEGDRDLDMNCTLPSPDOVVLVTEBGLYALNVLKNSLTHVPGIGAVQIYII 1665
QY      1615 KOLEKMLTAGERBALCVDVKKVQSLAOSHLPAQODISPMIPFAVKGCHLFGAGKIN 1674
DB      1666 KOLEKMLTAGERBALCVDVKKVQSLAOSHLPAQODISPMIPFAVKGCHLFGAGKIN 1725
QY      1675 GLCICAMPKSVIILRYNENLSKYCIRKEIETSEPCSIHFTNYSLIGTNKPYEIDMKO 1734
DB      1726 GLCICAMPKSVIILRYNENLSKYCIRKEIETSEPCSIHFTNYSLIGTNKPYEIDMKO 1785
QY      1735 YLIEEFLDKNDHSLADPAVFAASNSFPVSIYOVNSAGOREEYLLCFHEFGVFDYSGRS 1794
DB      1786 YLIEEFLDKNDHSLADPAVFAASNSFPVSIYOVNSAGOREEYLLCFHEFGVFDYSGRS 1845
QY      1795 RTDDLKMSRLPLAFAPREBYLFTVTHNSLEVEIQARRSAGTPARAYLDIPNRYLGPAI 1854
DB      1846 RTDDLKMSRLPLAFAPREBYLFTVTHNSLEVEIQARRSAGTPARAYLDIPNRYLGPAI 1905
QY      1855 SSGAIYLAASYODKLVICCKNLVYESGTEHHRGPSTSR 1894
DB      1906 SSGAIYLAASYODKLVICCKNLVYESGTEHHRGPSTSR 1945

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RESULT 3
US-09-804-471A-2
; Sequence 2, Application US/09804471A
; Patent No. 6479269
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: C1001164
; CURRENT APPLICATION NUMBER: US/09/804,471A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 497

```

TYPE: PR1
ORGANISM: Human
US-09-804-471A-2

Query Match 23.2%; Score 2430; DB 4; Length 497;
Best Local Similarity 99.1%; Pred. No. 1.3e-117;
Matches 464; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MUKFKYGANPLDAGAAEPDASRLNLFQCKPFPMTQOQMSPLSRGILDALFVLE 60
DB 1 MUKFKYGANPLDAGAAEPDASRLNLFQCKPFPMTQOQMSPLSRGILDALFVLE 60
QY 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEYQVREKATG 120
DB 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEYQVREKATG 120
QY 121 DIYAMKVMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFODKNHLYLMEYQPG 180
DB 121 DIYAMKVMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFODKNHLYLMEYQPG 180
QY 181 DLISLNRVEDQDENLQFYLAELILAVSHVMGYVRDIPKPNILVDRGHIKLVDF 240
DB 181 DLISLNRVEDQDENLQFYLAELILAVSHVMGYVRDIPKPNILVDRGHIKLVDF 240
QY 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVIAEMTYGR 300
DB 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVIAEMTYGR 300
QY 301 SPFAEGTSARTFNINMFORFLKFPDDPKVSSDFLDLIQSLCGQKRLKFBGLCCHPFF 360
DB 301 SPFAEGTSARTFNINMFORFLKFPDDPKVSSDFLDLIQSLCGQKRLKFBGLCCHPFF 360
QY 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFDEPKNSWSSPCQLSPGSGBELPFGVS 420
DB 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFDEPKNSWSSPCQLSPGSGBELPFGVS 420
QY 421 YSKALGILGRSESVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKM 468
DB 421 YSKALGILGRSESVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKV 468
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RESULT 4
US-10-238-709-2
Sequence 2, Application US/10238709
Patent No. 6680188

GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: CL001164DIV
CURRENT APPLICATION NUMBER: US/10/238,709
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 497
TYPE: PR1
ORGANISM: Human
US-10-238-709-2

Query Match 23.2%; Score 2430; DB 4; Length 497;
Best Local Similarity 99.1%; Pred. No. 1.3e-117;
Matches 464; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MUKFKYGANPLDAGAAEPDASRLNLFQCKPFPMTQOQMSPLSRGILDALFVLE 60
DB 1 MUKFKYGANPLDAGAAEPDASRLNLFQCKPFPMTQOQMSPLSRGILDALFVLE 60
QY 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEYQVREKATG 120
DB 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEYQVREKATG 120
```

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QY 121 DIYAMKVMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFODKNHLYLMEYQPG 180
DB 121 DIYAMKVMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFODKNHLYLMEYQPG 180
QY 181 DLISLNRVEDQDENLQFYLAELILAVSHVMGYVRDIPKPNILVDRGHIKLVDF 240
DB 181 DLISLNRVEDQDENLQFYLAELILAVSHVMGYVRDIPKPNILVDRGHIKLVDF 240
```

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QY 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVIAEMTYGR 300
DB 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVIAEMTYGR 300
QY 301 SPFAEGTSARTFNINMFORFLKFPDDPKVSSDFLDLIQSLCGQKRLKFBGLCCHPFF 360
DB 301 SPFAEGTSARTFNINMFORFLKFPDDPKVSSDFLDLIQSLCGQKRLKFBGLCCHPFF 360
QY 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFDEPKNSWSSPCQLSPGSGBELPFGVS 420
DB 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFDEPKNSWSSPCQLSPGSGBELPFGVS 420
QY 421 YSKALGILGRSESVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKM 468
DB 421 YSKALGILGRSESVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKV 468
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RESULT 5
US-09-804-471A-4
Sequence 4, Application US/09804471A
Patent No. 6479269

GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: CL001164
CURRENT APPLICATION NUMBER: US/09/804,471A
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 494
TYPE: PR1
ORGANISM: Mus Musculus
US-09-804-471A-4

Query Match 20.6%; Score 2165.5; DB 4; Length 494;
Best Local Similarity 87.8%; Pred. No. 5.2e-104;
Matches 411; Conservative 26; Mismatches 30; Indels 1; Gaps 1;

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QY 1 MUKFKYGANPLDAGAAEPDASRLNLFQCKPFPMTQOQMSPLSRGILDALFVLE 60
DB 1 MUKFKYGANPLDAGAAEPDASRLNLFQCKPFPMTQOQMSPLSRGILDALFVLE 60
QY 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEYQVREKATG 120
DB 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEYQVREKATG 120
QY 121 DIYAMKVMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFODKNHLYLMEYQPG 180
DB 121 DIYAMKVMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFODKNHLYLMEYQPG 180
QY 181 DLISLNRVEDQDENLQFYLAELILAVSHVMGYVRDIPKPNILVDRGHIKLVDF 240
DB 181 DLISLNRVEDQDENLQFYLAELILAVSHVMGYVRDIPKPNILVDRGHIKLVDF 240
QY 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVIAEMTYGR 300
DB 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVIAEMTYGR 300
QY 301 SPFAEGTSARTFNINMFORFLKFPDDPKVSSDFLDLIQSLCGQKRLKFBGLCCHPFF 360
DB 301 SPFAEGTSARTFNINMFORFLKFPDDPKVSSDFLDLIQSLCGQKRLKFBGLCCHPFF 360
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QY 361 SKIDMNNINSPFPVPTLKSDDDTSNFBPEKNSVSSPCOLSPSGFSGEELPFVGF 420
DB 360 AKDMNNINSPFPVPTLKSDDDTSNFBPEKNSVAFILCPABPLASGEEELPFVGF 419
QY 421 YSKALGILGRSSESVSGLDSPAKTSSMEKKLLIKSKELDSDQDKCHKM 468
DB 420 YSKALGILGRSSESVSSLDSPAVSSMEKKLLIKSKELDSDQDKCHKV 467

RESULT 6
US-10-238-709-4
; Sequence 4, Application US/10238709
; Patent No. 6680188
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: THEREOF
; FILE REFERENCE: CL001164DIV
; CURRENT APPLICATION NUMBER: US/10/238,709
; CURRENT FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-238-709-4

Query Match 20.6%; Score 216.5; DB 4; Length 494;
Best Local Similarity 87.8%; Pred. No. 5.2e-104;
Matches 411; Conservative 26; Mismatches 30; Indels 1; Gaps 1;

QY 1 MUKFYGARNPIDAGAAEPIASRASRLNLFQGGKPPMTQOOMSPLSREGIIDLALFVLF 60
DB 1 MUKFYGARNPIDAGAAEPIASRASRLNLFQGGKPPMTQOOMSPLSREGIIDLALFVLF 60
QY 61 EGSOPALMKIKHVSNFVRKYSDDTIAELOPSAKDFEVRSLVGGCHFAEVQVREKATG 120
DB 61 EGSOPALMKIKHVSNFVRKYSDDTIAELOPSAKDFEVRSLVGGCHFAEVQVREKATG 120
QY 121 DIYANKVMKKKALLAOEYVSFPEEBRNILSRSTSPWIPOLQYAFODKXHLVMEYQPG 180
DB 121 DIYANKVMKKKALLAOEYVSFPEEBRNILSRSTSPWIPOLQYAFODKXHLVMEYQPG 180
QY 181 DLSLNLNRYEDQDENLQFYLAELILAVSHVLMGYVARDIKPENILVDRGTGHIKLVDF 240
DB 181 DLSLNLNRYEDQDENLQFYLAELILAVSHVLMGYVARDIKPENILVDRGTGHIKLVDF 240
QY 241 GSAAKKNSKNVNAKLPITGTPDYMAPEVLTVNMEDRGTGILDCDMSVGVAVYEMVYK 300
DB 241 GSAAKKNSKNK-VDAKLPITGTPDYMAPEVLTVNMEDRGTGILDCDMSVGVAVYEMVYK 299
QY 301 SPFAEGTSARTFNINNFQRLKFPDDPVSSDPLDILSLCGOKERLKPGLCCHPFF 360
DB 300 TFFTEGTSARTFNINNFQRLKFPDDPVSSDPLDILSLCGOKERLKPGLCCHPFF 359
QY 361 SKIDMNNINSPFPVPTLKSDDDTSNFBPEKNSVSSPCOLSPSGFSGEELPFVGF 420
DB 360 AKDMNNINSPFPVPTLKSDDDTSNFBPEKNSVAFILCPABPLASGEEELPFVGF 419
QY 421 YSKALGILGRSSESVSGLDSPAKTSSMEKKLLIKSKELDSDQDKCHKM 468
DB 420 YSKALGILGRSSESVSSLDSPAVSSMEKKLLIKSKELDSDQDKCHKV 467

RESULT 7
US-09-916-204-2
; Sequence 2, Application US/09916204
; Patent No. 6638745
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
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; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: THEREOF
; CURRENT APPLICATION NUMBER: US/09/916,204
; CURRENT FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Human
US-09-916-204-2

Query Match 12.2%; Score 1277; DB 4; Length 257;
Best Local Similarity 99.2%; Pred. No. 1.3e-58;
Matches 250; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MUKFYGARNPIDAGAAEPIASRASRLNLFQGGKPPMTQOOMSPLSREGIIDLALFVLF 60
DB 1 MUKFYGARNPIDAGAAEPIASRASRLNLFQGGKPPMTQOOMSPLSREGIIDLALFVLF 60
QY 61 EGSOPALMKIKHVSNFVRKYSDDTIAELOPSAKDFEVRSLVGGCHFAEVQVREKATG 120
DB 61 EGSOPALMKIKHVSNFVRKYSDDTIAELOPSAKDFEVRSLVGGCHFAEVQVREKATG 120
QY 121 DIYANKVMKKKALLAOEYVSFPEEBRNILSRSTSPWIPOLQYAFODKXHLVMEYQPG 180
DB 121 DIYANKVMKKKALLAOEYVSFPEEBRNILSRSTSPWIPOLQYAFODKXHLVMEYQPG 180
QY 181 DLSLNLNRYEDQDENLQFYLAELILAVSHVLMGYVARDIKPENILVDRGTGHIKLVDF 240
DB 181 DLSLNLNRYEDQDENLQFYLAELILAVSHVLMGYVARDIKPENILVDRGTGHIKLVDF 240
QY 241 GSAAKKNSKNV 252
DB 241 GSAAKKNSKNV 252

RESULT 8
US-10-282-048-2
; Sequence 2, Application US/10282048
; Patent No. 6692948
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: THEREOF
; FILE REFERENCE: CL001164CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/282,048
; CURRENT FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Human
US-10-282-048-2

Query Match 12.2%; Score 1277; DB 4; Length 257;
Best Local Similarity 99.2%; Pred. No. 1.3e-58;
Matches 250; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MUKFYGARNPIDAGAAEPIASRASRLNLFQGGKPPMTQOOMSPLSREGIIDLALFVLF 60
DB 1 MUKFYGARNPIDAGAAEPIASRASRLNLFQGGKPPMTQOOMSPLSREGIIDLALFVLF 60
QY 61 EGSOPALMKIKHVSNFVRKYSDDTIAELOPSAKDFEVRSLVGGCHFAEVQVREKATG 120
DB 61 EGSOPALMKIKHVSNFVRKYSDDTIAELOPSAKDFEVRSLVGGCHFAEVQVREKATG 120
QY 121 DIYANKVMKKKALLAOEYVSFPEEBRNILSRSTSPWIPOLQYAFODKXHLVMEYQPG 180
DB 121 DIYANKVMKKKALLAOEYVSFPEEBRNILSRSTSPWIPOLQYAFODKXHLVMEYQPG 180
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QY	18	DLSTLNRYEDQDQDENLIGFYLAELLIAVSHVLMGYHARDIKPENILVDRGTGHIKLVD	240
		DLSTLNRYEDQDQDENLIGFYLAELLIAVSHVLMGYHARDIKPENILVDRGTGHIKLVD	240
Db	181	DLSTLNRYEDQDQDENLIGFYLAELLIAVSHVLMGYHARDIKPENILVDRGTGHIKLVD	240
QY	241	GSAAKNNNNNNV	252
		GSAAKNNNNNNV	252
Db	241	GSAAKNNNNNNV	252

RESULT 9
US-08-68

Sequence 1, Application US/0865576
Patent No. 5906819
GENERAL INFORMATION:
APPLICANT: Kaibuchi, Kozo
APPLICANT: Iwamatsu, Akihito
APPLICANT: Nakano, Takeshi
APPLICANT: Ito, Masaaki
APPLICANT: Takahashi, No. 5906819uaki
TITLE OF INVENTION: RHO TARGET PROTEIN RHO-KINASE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D C
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,576
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-325129
FILING DATE: 20-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-17150
FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-131206
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16887/843
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1388 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-685-576-1

Query Match	11.9%	Score 1253;	DB 2;	Length 1388;
Best Local Similarity	26.1%;	Pred. No. 1.4e-56;		
Matches 394;	Conservative 291;	Mismatches 507;	Indels 320;	Gaps 50

[illegible]

Db	67	NIDNIFLARIYEKIVYKKGIRGLQMAKEDVDVNVYVIRGAFGEVQVLRHKAQOVVAMKULSKFE	126
Qy	132	ALLAEOVSFPFEERBNILSRSTSPWIPOLQYAFQDKNHLTYMEYOQGDLSILNRYED	191
Db	127	EMIRSDSAFMEBERDIMAIPANSFPWVQLCFACQODDKYLVYMWVEYFGGLVAINMSNYD-	185
Qy	192	QUDENLQFYLAELILAVHSHVMGYVHRIPKENTILVDOTGHIKLVDFPSAAKNNSMK	251
Db	186	-VPERMAKFYAEVAVLLADLAISHGLHVRVYKPDNNLLDNGHUKLADPCTCMKDBETGM	244
Qy	252	VNAKLPICTPDYMAPEVLTVMNGDGKGTGYGDCDWMVSVGIAYEMIYGRSPFAEGTSART	311
Db	245	VHCTAOTGTPRYITPEYVYKSGQGD--GYRECDWMVSUGVFLPEMLVGDTPYFVADSLVGT	302
Qy	312	FNNIMNFQFLKFPDDPKVSSDFLDLIQSLICQOKERLKEG--LCSPFEKIDWN--	366
Db	303	YSKIMDHKNSLCPEDAEISGHANLILCAFLTREVALYGRNGVEIYKOPHFPFNDOQMND	362
Qy	367	NIRNSPPFPVYTLKSDDDTSNPDPEKNSM-VSSPCQLSPSGSGSELPFVFPYSYKUL	425
Db	363	NIREPAAVVEBELSSDIDSNPDDIEDQKDVLEFP--PKAFVGNOLFFIGFTTYREN	419
Qy	426	GILGRSEVSVGLSPSPA--KTSMSERKLLIKSKELQSDQDKCHMEQEMTLRHRVSEVE	483
Db	420	ILLS-----DSPCKENDISQSR--KNESQGEIQKKVLTYEHLN-----	457
Qy	484	AVLSQKEVELKASTORSLLFODIATYITECSSIKLSLEQARNEVSOEDDKALQOLHDIR	543
Db	458	-----TEIQAKEE-----LEQ-----KCKSVNTELEKVAKELEBEITLRKNVESTLR	499
Qy	544	--EQSKLOELKEBOYQOVBEHMLNMNOLEEDIVSARRSDYSESLRESRLAAEFKR	601
Db	500	QLERKALLQHKNAEYOQKADHEADKRRNLBNVNSLKQDLEDIKKRQNSQISTE----	555
Qy	602	KATCQNHLLYAKQCKREVEGEVAKELINAEQOLKIQ-----ELQEK--LEKAKER	652
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Qy	653	AERELEKQNRNEDSSEGIKKULVAEERRRSLNENKVRLETMERRENRLKODIOTSQOI	712
Db	616	LEKEPINOVSLESE--RRDRTGSETINDLOGRISGLEBEDVNGKILLAKVLELEKQOL	672
Qy	713	QOMADKILELEKREAOVSAQH-----LYNHLKXE-QHYBEKIKVLD-NOIKYDL--AD	764
Db	673	Q---ERFIDLEKEKNNMEIDMTYQVKVIAQOSLEQEBETHKATKRLADKKNKIYESIEAK	729
Qy	765	KETLENNMQRHEEBAHEKGI--LSEQKAMINAMDSKISLEORIYELSE---ANKLA	817
Db	730	SEAMKEMEKUSSEERTLKQYENLLEBKRCSTLDDODKQSQKINELLKQKOVANEDV	789
Qy	818	ANNSI-----FTQRNKAQOEBMISBLROOKFYLETQAGLEKQNRKLEBQLEKIS	867
Db	790	RULTLIKIHOETQKRCLTQNDLKMOTQOVNLTAKMS-----EKOLQO--	829
Qy	866	HODHSDKRLLELETRLEVEVLEHHEQKLETKQOLTELQSLQJERESQOLTALQARAALF	927
Db	830	-----ENNHLLEMKSL-----EKONABIRKEROQDOGOMKELQOULEABOYFSTLYK	877
Qy	928	SOLROAKTELEBTT--AEAEIEIOALTANHDEIQKFPDALRNSCTVITDLEBOLNOLTE	984
Db	878	TOVRELKECEBKTKLCELOQKQOELDERDSLAQLE-----ITLTKADSEQLAR	929
Qy	985	DNAELINNONFYLSKQLEASGANDEIYOJLRSEVDHLRREITEREMOULTSQOJMEALKTT	1044
Db	930	SLAEQOYSDLEKEKIMKE-----LEIKEMMARHKOELTEKADATIASLEETNRILTSD	981
Qy	1045	CTMLEBOVMDLEALNDELLEKEROEAMRSTVSGE-----KOFERVPELORMIDTE	1097
Db	982	VANILAN-----EKXEILNNKLEAQEO--LSRLKDEEISAAIKQAF-----KOLITE	1027
Qy	1098	KQSRBARADORITESHQOVAVLEVKHKAETIILLOALKEQKLAESLSDKLNLEKKAJML	1157
Db	1028	RTLKTOAVNKL-----AEINRKAKEPVK-----RGNDTIVRKK--	1059

Qy	1158	BMNARSLOQKJETSEBELKQRLLEBQAKJQOQMDLOXNNIPLYTO---	GLQALBRADLYK	121.4
Db	1060	EKENRKHLMELKSERE---KLTOOMIKYQKELNEMOAOIAEBSQIRIQLMTLSSKD---	1113.3	
Qy	1215	TERSDLEXYOLENIOVLY-----SHEKVMEGTIS---	QOTKLIDF	1251
Db	1114	---SDIEBLRQLOALNHGLBSSSTIGSGPGDTEADGFPESRLEBQWLSPLRYNNITKKRGW	1170	
Qy	1252	LQAKMDOPAKKKKGJFSRKEDPALPTYO-----PLYNELKLALEREKARCAEL	1301	
Db	1171	VKATVYVSSKKILFYDSQDKEQSNPYWVLIDKLFHVRPTYQTOVYNADAKELPRIGQI	1230	
Qy	1302	EEALQKTRIELRSAREBAHRRKATDHPHSPRTATARQOIAMSAIVSPEHOPSAMSLAP	1361	
Db	1231	-----LYAN	1234	
Qy	1362	PSRRKESSTP---EFSRRLKERMMHNIPIHRPVNGJLMBATKCAVCLDTVYHGORQSK	1417	
Db	1235	EGESKKEDEFPVEPVGKSNYIICHKGHEFIPLYNH-----PTWCEACMKRLMHMFKPP	1289	
Qy	1418	CLECOVMCHPKC	1429	
Db	1290	ALBGR-RCHIKC	1300	

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1  RESULT 10
2  US-08-685-871-2
3  Sequence 2, Application US/08685871
4  Patent No. 6013499
5  GENERAL INFORMATION:
6  APPLICANT: NARUMIYA, Shuh
7  APPLICANT: IWAMATSU, Akhiro
8  TITLE OF INVENTION: RHO TARGET PROTEIN KINASE P16
9  NUMBER OF SEQUENCES: 68
10  CORRESPONDENCE ADDRESS:
11  ADDRESSEE: Foley & Lardner
12  STREET: 3000 K Street, N.W., Suite 500
13  CITY: Washington
14  STATE: D.C.
15  COUNTRY: USA
16  ZIP: 20007-5109
17  COMPUTER READABLE FORM:
18  MEDIUM TYPE: floppy disk
19  COMPUTER: IBM PC compatible
20  OPERATING SYSTEM: PC-DOS/MS-DOS
21  SOFTWARE: PatentIn Release #1.0, Version #1.30
22  CURRENT APPLICATION DATA:
23  APPLICATION NUMBER: US/08/685,871
24  FILING DATE: 24-JUL-1996
25  CLASSIFICATION: 435
26  PRIOR APPLICATION DATA:
27  APPLICATION NUMBER: JP 8-184102
28  FILING DATE: 25-JUN-1996
29  PRIOR APPLICATION DATA:
30  APPLICATION NUMBER: JP 7-262553
31  FILING DATE: 14-SEP-1995
32  ATTORNEY/AGENT INFORMATION:
33  NAME: BENT, Stephen A.
34  REGISTRATION NUMBER: 29,768
35  REFERENCE/DOCKET NUMBER: 16887/845
36  TELECOMMUNICATION INFORMATION:
37  TELEPHONE: (202)672-5300
38  TELEFAX: (202)672-5399
39  TELEX: 904136
40  INFORMATION FOR SEQ ID NO: 2:
41  SEQUENCE CHARACTERISTICS:
42  LENGTH: 1354 amino acids
43  TYPE: amino acid
44  TOPOLOGY: linear
45  MOLECULE TYPE: protein
46  US-08-685-871-2

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Query Match	11.9%	Score 1250.5	DB 3	Length 1354
Best Local Similarity	26.0%	Pred. No. 1.8e-56		
Matches	393	Conservative	298	Mismatches 543
			Indels	275
			Gaps	51
QY	44	SPLSRREGILDALFVLFEECSQAPALMKIKGNVFNVRKYSDTIAELOELPSAKDEVRSLV	103	
DB	23	SEVNSDCLDLDDALVYDLDPPALRKNNKINIDNFLSRYDITINKIRDLRMKADEYEVVAVI	82	
QY	104	GCCHFAEYQVYREKATGDIYAMKMKKALLAQSOVSFFEEERNILSRSTPWIPOLOYA	163	
DB	83	GRGAFGEVQLVRHKSTRKTVYAMKLLSKFEMIKRSDSAFFWEERDIMAFAVNPVWOLPYA	142	
QY	164	FODKNHLYMEBXOQGDLLSLMRBYEDQDENIIOFLAELILAHVSVHLMGVYHPIK	223	
DB	143	FODRYYLVMWEMYPGGDLVNLMSNYD--VEKARFPTAAVVALDILHSMGFLHRYVK	200	
QY	224	PENILVDRTGHIKIVDFGSAKNNKNNKVNKACLIGTPDYAPAVLYTMNDSGKQYGLD	283	
DB	201	PDMNLDRKSGHKLADRGTCMKNNKEGVNRCDTAVGTPDIISPEVLVSGQGD--GYVORE	258	
QY	284	CDMWSVGIAYEMIYGRSPFAEGTSARTFNNINMFQRELPKDDPKVSSDFLDLIQSLLC	343	
DB	259	CDMWSGVFLYEMLVGDPFYADSLVGYTSKIMNHKNSLTPDDNDNISKEAKNIIICAFYI	318	
QY	344	GQKRLIKREG--LCNPFPSKID--WNININSPPFPYTLKSDPDNNSPDEPEKNWSV	398	
DB	319	DREYRLGNNGVEEIKRHLFFNDQWAMETLLDTPAAPVDPDLSIDITNSFDLEKDEE	378	
QY	399	SS-PCQLSPSGSEBELPFGVFSYSKALGILGRSESVSGDSDPAKTSMEKKLLIKSE	457	
DB	379	ETFPF---PKAFVGNQPLPFGVFTY---YSNRYYLSSANPNDRNRSN-----ADKS	423	
QY	458	LQDS--QDCKHMEQMTLRHVRVSEVAVLQKEVELKASETOR---SLBED--LATYIT	512	
DB	424	LQESLQIKTYLXEBQL-----HNEMQLKDEMEQCRITSNIKLDIKIMKELD	468	
QY	513	ECSSLKSLSEQARNEVSGEDDKALQILHDIREQSKLOEIEGEYQAOVE--EMRLMNQOL	571	
DB	469	EEGNQRRLNET---VSQIEKEMKLLQHRINEYORKAQ--ENSKRRRVENEVSTLLKQOL	523	
QY	572	EDLVASARRRDVLESSELRESRLAAEFKRKATGCONHLYLAKQOGRVEGEVAMLEKIN	631	
DB	524	EDLKTVSONSOL-----ANF---KLSQLQKOLEANDILRTRESTPAVRLKSH	568	
QY	632	AEQOLKIOELOEKLEKAKERARELEKLONRDESSBEGIKLVEABERRHSLENNKVL	691	
DB	569	TEWKSISQL--ESLNRELQER--NIILENSKSGQTOKDYQOLAILAEBERDNG-----	618	
QY	692	ETMERRENRLKODIQTK---SQOIQQMADKILELBEKGRBAQVSAOHLVNLKQKQEHY	747	
DB	619	-----HSEMIIGDLQARTITSLOEEVVKHLKNHLEVEGERKEQAOMLNHSE---KEK---	666	
QY	748	EKKIKVLDNOIKKOLADKETLENNMQHREBAH-----KGILSEBQAKMIAMMSKIRSL	803	
DB	667	-----NNLEIDILNYK--LKSIIQQRBOGVNHNKVTYKALTLKHOSIEBAKSVANCEM	716	
QY	804	EORIVELSEAKRLAANSLSLFTQPMKMAQOEIMIS--ELRQKUYELTQAGKLEAQRNKLKEO	862	
DB	717	EKKIKEREBARAKENRVV---QIEKQCSMLVDVLKQSOQKLEHITGNKE---RMBDE	768	
QY	863	LEKISHQDSHDKNRLLELTRLEVSLSEHBEQK-----LELKRQLTLOLS-	908	
DB	769	VKNITTLQLEGSSNRKLLIQLLOKTAQFAEADYLKGLKQMKOQEIWTLLEAKR--LLEFELIAQ	827	
QY	909	-----LQRESQULTLOQAAABALBESQLQKATLEETTALEBEETIQAALTANDE	957	
DB	828	LTKOYRGNEGQRELOQLEAQFSTLYKQVEXLEKEELBEKRENNIKKIOELQNEKET	887	
QY	958	IQRKFDALRNSCTYITDLBQLOANDTEDNAELNNQNFILSKQOLDEAGANDIEIVOLRSEV	1017	
DB	888	LATQUD-----LAETKASEQDA--RGLLEQYIELTQESKKAASRN-----	927	
QY	1018	DHLREITEREMQUTSQKQWMAELKTTCTMLEBQVMDLEALNDELLEKQERQEMARSVLG	1077	

Db 928 ---ROEITDKD-----HTVSRLFEANSMLTKOIEILRRNEBELTEKCKAEEBYKLEK 977
Qy 1078 DE-----KSQECRVRELOQMLDTEKOSBARADQRTSROVVELAVENHKAELIALQQA 1112
Db 978 EEEISNLKNAFE-----KNINTERTLTKTOAVNKLAEIMNKDKPKIRKKAANTODLKK 1030
Qy 1133 LKEOK---LKASLSLDPKLNDEKKAAMLENNARSLOOKLETREBELKORLLEEOA---KLQ 1186
Db 1031 EKENRKLQLELNOERKEKQVYVKA-----QKEL---NDMQAOVLVECAHRELQ 1077
Qy 1187 OQMDLOKNIHFRITQLOALDRADLLKTERSDELOENIOVLYSHEKYMKEGITISQOT 1246
Db 1078 MQLASKESEDIOQRATLLDSDTSVASPSAD-----ETDGMLEPSR 1120
Qy 1247 KLIDFLOAKMDOPAKKKGLFSSRKEDPALPPOVPLQVNEKLALKEKARCALHEALQ 1306
Db 1121 -----TEGMLSVNRRNIRKYGWKQYVVSSKILFYNDEODKEQSNPSMTLIDKL-- 1173
Qy 1307 KTRIELRSAREEAHRAKATDHPHSTPATAROOIAMSATVRSPEHOPASMSLLAPSSRR 1366
Db 1174 ---FHRPVTQGVVYAAET-----EEIPKIFQILVANEGERC 1206
Qy 1367 KESSTPEESFRRLKERHNIHPIRENVGLMNRATKCAVCLDVIHFGROASKLEQVWCH 1426
Db 1207 RKDVEBPVQQAQEKTFQNHKGHEFTPLYHPPANDACAKPLMHVFKPRPALBECK-RCH 1265
Qy 1427 PKGS-----TCLPATCGLPAAVATHTFAFCRDKMNSPGLQTKPESSSLHEGMM 1476
Db 1266 VKGRDHLDKKEDLIC-----PKVSYDVYTSR--RDMILLACSDDEQKQWTVHLV--K 1314
Qy 1477 KVPNNNRKG 1485
Db 1315 KIPKNPPSG 1323
RESULT 11
US-09-976-594-296
; Sequence 296, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 296
; LENGTH: 1388
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673549 064987CD1
US-09-976-594-296
Query Match 11.9%; Score 1249.5; DB 4; Length 1388;
Beet Local Similarity 26.3%; Pred. No. 2.1e-56;
Matches 391; Conservative 291; Mismatches 513; Indels 293; Gaps 47;
Qy 24 ASRLNLPFGQKPPMTQOQMSPLSRGILDALFVLFECSQPALMKITGVNSNFPKXSDT 83
Db 24 ASR-----QRKLEALIRDRSPINVESLIDGLNSLVLDLDFPALRKNNKINIDFNARVEKI 78
Qy 84 IAELOELQPSADFEVRSIVGCGHFAVQVREKATGDIYAMKVKKKKALLAOEVSFFE 143
Db 79 VKKIRGLQKADYDVVKVIGRGAFGEVULVNHKKSQKYAMKLSKSTEMIKRSDSAFW 138
Qy 144 EERNILSRSTSPWIPOLQYAFODKNHLYLMEBYQDGDLLSLNRYEDQDLNLIQFLA 203

Db 139 EERDILAFANSPWVOLFYAFODDKRYLYVMMEYMGDLYNLSMYD--VPEKAKFYTA 196
Qy 204 ELILAVSHVLMGYVRDIKPNILVDTGTGILKYDFGSAAGNSNKNVYNALPIGTDPY 263
Db 197 EYVLALDAHSWGLJHRVYKPDNMLLDKKGHLKLDFFGCMQMDGTGWHCTYAGTDPY 256
Qy 264 MAPEVLTWNGDGKGTGYLDGCMWSGVYAYEMIYGRSPFAGTSARTEFNINNFORFLK 323
Db 257 ISPEVLKSGQGD--GGYGECDMWSVGFLEYMLVGDTPFYADSLVGTYSKIMDHKNSLC 314
Qy 324 FPDQPKVSPDFLLIOSLLCGQKERLKFEG---LCCHPFF--SKIDWNINRNSPPFVYT 378
Db 315 FPEDAISKAKNLICAFILDRVLRGNGVEIRQHPPEKIDQWMDNIRETAAPVVE 374
Qy 379 LKSDDTSNFDEPKNSW--VSSPCQSPSGFGEELPVGVSYSKALGILGRSESVG 437
Db 375 LSSDIDSSNPDIDEDGDVETFPPI---PAFVGNQLPFIQFTYRENILLS----- 423
Qy 438 LDSPA--KTSMEKULLIKSKELQDSQDKCHKMEOEMTRLHRRVSEVAVLQGEVELKA 495
Db 424 -DSPSCRENDSTQGR--KNBESQETQKLYTEHLSN-----EMQA 462
Qy 496 SETQSRLLBODLATYITEGSSLSRLEQARMEVSQ-----DKALQLLHDIREQRL 549
Db 463 KEE---LEQ-----KCKSVNTRLEKTAKELEBEITLLKSVESALROL---EKKAL 507
Qy 550 QETQEQYQAVCEMRMLMNQLEEDIVSARRSDVLESELRESRLAAEFKRAKTEQHK 609
Db 508 LQHKNAEYQRRADHEADKKNLENVNSLKQLEBDLKKQNSQISTE---KVNDLQRO 563
Qy 610 LKAKDQGPVEGVAYLKEKINAEQOLKIQ-----ELOEK--LEKAKERARELEKU 660
Db 564 LDETNALLRTESDPAARLARKTOAESKQIOLESNNMDLDQKCLLETALKLEKEFINL 623
Qy 661 QNRDSSGRTKULVEAEERHSLNKNVYKLETERENRKLKODIOTKSQOIOOMADKIL 720
Db 624 QSALESE---RRDRTHGSEIINDLOGRICGLEBDLKNGKILLAKVELBKQLOERFPD-L 679
Qy 721 ELEEGHRAOVSQAQ--HLEVALKQKE--QHYEEKIKVLD-NOIKKDL--ADKETLENNMOR 774
Db 680 EKEKSNMEIDMTYQKVIQSLQEBAEHKATKARLADKNKIYSIEAASNAKMEKK 739
Qy 775 HEEBAHEKGI--LSEQKAMINAMDSKIRSELBOIYELSANLTLANSLSFTQNNKAQ 831
Db 740 LIEERTLKQKVENILLEAEKRCSTLDCLOKSOQKINEL-----LKOK 782
Qy 832 EEMISELAQOKFYLETQAGKLEAQNRLKEBOLKISHODHSDKNRLLELTRLEVSLEH 891
Db 783 DVLNEDVNRNLTIKIETQKCCLTQNDLAKMTQOVNTLKASEK-QLQENNHLMEMKGNL 841
Qy 892 EEOKLELKKOLTELQSLQERESQTLTALOARALLESQLOAKTELETT--AAEAEI 948
Db 842 EKQNAELKREKRDADQGMKELODQLEAQVSTYKTVBELKECECEKTKLQKRELQKK 901
Qy 949 QALTARDEIQKFPALANSCTVITDLEQNLUTEDNAELNNOVFYLSKOLDEASAND 1008
Db 902 OELODERBILAQLR-----ITLTADSQBLARSTAEQSYDLEKTKMKE----- 947
Qy 1009 EIVOLRSEVDNLRREITEREMQTSQKOTMEALKTCTMLEBOVNDLEALNDELIEKQ 1068
Db 948 --LEIKEMARKQOELTEDATIASLEETNRFLTSDVANLAN--EKEELNNKLQDVOEQ 1002
Qy 1069 WEAMRSVLDE-----KSQECRVRELOQMLDTEKOSBARADQRTSROVVELAVENH 1121
Db 1003 ---LSRLKDEIEISAALIAQFE-----KOLTERTLKTQAVNKL----- 1038
Qy 1122 HKAEILLALQALKEQGLXABSSDLKLNDEKKAAMLENNARSLOOKLETREBELKORL 1181
Db 1039 --AEINNRKEPVK-----RNDPDVYRK--EKENRKLHMEKLSERE--KLQO 1080
Qy 1182 QAKLQOQMDLOKNIHFRITQ---GLQALDRADLLKTERSDELOENIOVLV----- 1231


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Oy      1069 WEAMRSVLGDE-----KSOFECRVRELORMIDTEKOSRARADQRTESQVVELAVEK 1121
Db      1003 ----LSRLDEBISAIAKAQFE-----KQLTERLTQAVNKL----- 1038
Oy      1122 HBAEILALQALKEQCKAKESISDKLNDLEKKNHLEMARBLQCKLTERELKORLLEE 1181
Db      1039 --AEIWRKRPVK-----RGNDYVRRK--EKENRLKHELSERE---KLTYQ 1080
Oy      1182 QAKLQOQMLQKNHIFRLTY---GLQELDRADLKTESRDIEYOLENIQVLY----- 1231
Db      1081 MKTYQKELBEMQALBESQIRLEQMTDSKD-----SDIQLRSQQAHLIGLSDSS 1134
Oy      1232 -----SHEKVMETIS---OQTKLIDFLQAKMDQPAKKKGLFSRREKDBA 1275
Db      1135 ISGPGDAEADDFEPSRLGMLSLPVNNTKKFGVKKYLVSSKKILFYSEODKEQS 1194
Oy      1276 LPTQV-----PLQYNELKLALBKKARCAELBMLQKTRIELRSAREBAHRKAT 1325
Db      1195 NPYVVLIDIDLFFHVRPVYTQTDVVRADAKETPRIFQI----- 1230
Oy      1326 DHPHSTPATARQOIMSAIVRSPEHQPMSMLAPPSSRRKESSTP---EFSRRLKE 1381
Db      1231 -----LYANEGSSKKQEFPPVPEVGEKSNYICH 1258
Oy      1382 RMHNIPIHRENVGLNMRATKCAVCLDTVHFGQASKLECCQVCHPXC 1429
Db      1259 KGHFIPTLYHF-----PTNCEACMKPLMHMFKRPALBCR-RCHIKC 1300

RESULT 13
US-09-916-204-4
; Sequence 4, Application US/09916204
; Patent No. 6638745
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO01164CIP
; CURRENT APPLICATION NUMBER: US/09/916,204
; CURRENT FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-916-204-4

Query Match      11.2%; Score 1173; DB 4; Length 251;
Best Local Similarity 90.0%; Pred. No. 2.9e-53;
Matches 226; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

Oy      1 MLKKYAGARNPLDGAABPIASRASRLNLFQGKPPMTQOQMSPLSREGILDALFVLFE 60
Db      1 MLKKYGVARNPSEASAPPIASRASRLNLFQGKPPMTQOQMSALSREGVLDLFLVLE 60
Oy      61 ECSOPALMKIKHVSFVAKYSDTIAELQELQPSAKDEVSRLVCGHFAEVQVVRKATG 120
Db      61 ECSOPALMKIKHVSFVAKYSDTIAELRELQPSVRDEFVRSVLVCGHFAEVQVVRKATG 120
Oy      121 DIYAMKVKKALLAQBQVSPFEERNTLSRSTSPWIPOLQYAFQDKNKLYLMEYOPGG 180
Db      121 DVIYAMKIMKKAALRAQBQVSPFEERNTLSQSTSPWIPOLQYAFQDKNKLYLVMEYOPGG 180
Oy      181 DLSLNNRYEDQDENLQFYLAELILAVSHVHLMGVYHRDIKENTILVDRTHIKLVDF 240
Db      181 DLSLNNRYEDQDENMLOFYLAELILAVSHVHMGVYHRDIKENTILIDRTGHIKLVDF 240
Oy      241 GSAAKMNSNM 251

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Db      241 GSAAKMNSNM 251

RESULT 14
US-10-282-048-4
; Sequence 4, Application US/10282048
; Patent No. 6692948
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO01164CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/282,048
; CURRENT FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-282-048-4

Query Match      11.2%; Score 1173; DB 4; Length 251;
Best Local Similarity 90.0%; Pred. No. 2.9e-53;
Matches 226; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

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Db      61 ECSOPALMKIKHVSFVAKYSDTIAELRELQPSVRDEFVRSVLVCGHFAEVQVVRKATG 120
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Db      121 DVIYAMKIMKKAALRAQBQVSPFEERNTLSQSTSPWIPOLQYAFQDKNKLYLVMEYOPGG 180
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Oy      241 GSAAKMNSNM 251
Db      241 GSAAKMNSNM 251

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; Sequence 5, Application US/09916204
; Patent No. 6638745
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO01164CIP
; CURRENT APPLICATION NUMBER: US/09/916,204
; CURRENT FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-916-204-5

Query Match      11.2%; Score 1170; DB 4; Length 251;
Best Local Similarity 89.6%; Pred. No. 4.1e-53;
Matches 225; Conservative 16; Mismatches 10; Indels 0; Gaps 0;

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Db      61  ECSQPALMKIKGVSNFYRKYSDTTIAELQEIQPSAKDFEVRSLVCGHFAEVQVVRKATG 120
Qy     121  DIYAMKVMKKKALLAQEOVSFFEEERNILSRSTSPWIPOLQYAFODKXNLXLMEXOPGG 180
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Qy     181  DLSLNLRYEDQDENLIQFYLAELILAVSHVLMGVHRDIKPENILVDRTGHIKLVDF 240
Db     181  DFLSLNLRYEDQDENLIQFYLAELILAVSHVLMGVHRDIKPENILVDRTGHIKLVDF 240
Qy     241  GSAAKMNSNM 251
Db     241  GSAAKMNSNMV 251

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 Job time : 60 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 27, 2005, 13:45:16 ; Search time 203 Seconds

(Without alignments)
3317.613 Million cell updates/sec

Title: US-10-017-216-2

Perfect score: 10490
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Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	10480	100.0	2053	14	US-10-325-430-12
3	10490	100.0	2053	16	US-10-757-262-52
4	10032.5	95.6	2054	13	US-10-415-011-21
5	10022.5	95.5	2054	13	US-10-028-946-2
6	10011	95.4	2055	16	US-10-618-941-67
7	10007	95.4	2066	11	US-09-964-956-9
8	10007	95.4	2066	15	US-10-262-511-14
9	10005	95.4	2053	11	US-09-964-956-11
10	10005	95.4	2053	15	US-10-262-511-2
11	9487.5	90.4	2055	13	US-10-017-216-4
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13	7717.5	73.6	1641	11	US-09-964-956-40

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15	7491.5	71.4	1597	11	US-09-964-956-41	Sequence 41, Appli
16	7491.5	71.4	1597	13	US-10-017-216-6	Sequence 6, Appli
17	6745.5	64.3	1441	15	US-10-412-897-3	Sequence 3, Appli
18	6223.5	59.3	1286	11	US-09-964-956-38	Sequence 38, Appli
19	6223.5	59.3	1286	13	US-10-017-216-7	Sequence 7, Appli
20	4718.5	45.0	999	15	US-10-276-774-1487	Sequence 1487, Ap
21	4519.5	43.1	940	11	US-09-964-956-39	Sequence 39, Appli
22	4249.5	40.5	883	11	US-09-964-956-37	Sequence 37, Appli
23	4101	39.1	847	15	US-10-262-511-8	Sequence 8, Appli
24	4005.5	38.2	832	15	US-10-262-511-6	Sequence 6, Appli
25	3155	30.1	623	15	US-10-262-511-4	Sequence 4, Appli
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34	2165.5	20.6	494	15	US-10-724-594-4	Sequence 4, Appli
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39	1421.5	13.6	1719	15	US-10-362-892-2	Sequence 2, Appli
40	1400	13.3	1738	15	US-10-210-130-100	Sequence 100, App
41	1399.5	13.3	1664	15	US-10-210-130-102	Sequence 102, App
42	1383.5	13.2	1711	17	US-10-781-581-206	Sequence 206, App
43	1382.5	13.2	1711	9	US-09-771-161A-219	Sequence 219, App
44	1382.5	13.2	1711	9	US-09-771-161A-220	Sequence 220, App
45	1382.5	13.2	1711	15	US-10-399-225-10	Sequence 10, Appli

ALIGNMENTS

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US-10-017-216-2
; Sequence 2, Application US/10017216
; Publication No. US20020160483A1
; GENERAL INFORMATION:
; APPLICANT: KAPILLER-LIBERMAN, Rosana
; TITLE OF INVENTION: 13345, A No. US20020160483A1et Human Myotonic Dystrophy Type Pro
; FILE REFERENCE: 10147-57U1
; CURRENT APPLICATION NUMBER: US/10/017,216
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/242,429
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2053
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-216-2

Query Match      100.0%; Score 10490; DB 13; Length 2053;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2053; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      61 EESQALMKIKRVSNFVKRYSPTIAELQELQPSADPEFVRSLVGGCHRAEVOVREKATG 120
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DB      121 DIYAKWKKKKLLAQEOVSFFEEERNILSNSTSPWIPOLQYAFODKXHLVLMEEYOPGG 180
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RESULT 2
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; Sequence 12, Application US/10325430
; Publication No. US20030153525A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Rosenfeld, Julie Bech
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
; FILE REFERENCE: MP101-294P1BM
; CURRENT APPLICATION NUMBER: US/10/325,430
; PRIOR APPLICATION NUMBER: US 60/341,953
; PRIOR FILING DATE: 2001-12-19

NUMBER OF SEQ ID NOS: 21
 SOFTWARE: Faeseq for Windows Version 4.0
 SEQ ID NO 12
 LENGTH: 2053
 TYPE: PRT
 ORGANISM: Homo Sapiens
 US-10-325-430-12

Query Match 100.0%; Score 10490; DB 14; Length 2053;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matched 2053; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 721 ELBEKREARQVSAQHEVHLKQKQHYEEKIKVLNQIKKDLADKKTLENNMORHEEAAH 780
 781 EKGKILSEQKAMINAMDSKIRSLQRIVELSEANKLAANSJLFTQNMKAQOEEMISELKO 840
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 841 QKFYLETQAGKLAQNRKLEBQLEKISHODHSDKNLLETLRLRVSLEHEQOKLELR 900
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901 QTELOLSQERESQUTALQAARALLESQLRQAKTELETTAAAESEIQALTNRDEIOR 960
 961 KFDALRNSCTVTLDLEQNLQUTEDNAELNQNPLYSKQLDASGANDIYOLRSFVHL 1020
 961 KFDALRNSCTVTLDLEQNLQUTEDNAELNQNPLYSKQLDASGANDIYOLRSFVHL 1020
 1021 RREITEREMQLSQKQTMALKTTCMLEEQVMDLEALNDELBEKROEAWRSVLDGDK 1080
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 1081 SQFECHVRELQMLDTEKOSRARADQRTESQVVELAVKEKABITLALQALKEQKXLA 1140
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 1141 ESLSKDLNDELKXHAMLENARSLOQKLETERELQRLLEBOAKLQOQMDLQKNIIFRLT 1200
 1201 OGLQELADRADILKTERSDLEYQLENIOVLYGHEKVQMGTTISOOTKLDPLQAKMDQPA 1260
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 1261 KKKKGLFSRKKEDPALPTQVPLQVNEKLALKEKARCALEBEALQKTRIELRSAREEA 1320
 1261 KKKKGLFSRKKEDPALPTQVPLQVNEKLALKEKARCALEBEALQKTRIELRSAREEA 1320
 1321 HRKATDHPHSTPATARQOIASAIVRSPEHOPASMSLIAPSSRRKESSTPEBFSRLK 1380
 1321 HRKATDHPHSTPATARQOIASAIVRSPEHOPASMSLIAPSSRRKESSTPEBFSRLK 1380
 1381 ERMHNHNPFRFVNGIMPAITKCAVCLDPTVHFRQASKCLECQVMCHPKSTCLPATCGP 1440
 1381 ERMHNHNPFRFVNGIMPAITKCAVCLDPTVHFRQASKCLECQVMCHPKSTCLPATCGP 1440
 1441 AEYATHTFAFCRDKNNSFGLOTKEPSSSLHLEGMMKYPNNKRGQOQWDRKYIVLEGSK 1500
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 1561 KLEGDRLDMNCTLPSPDOVVLVGTBEGLYALNVKNSLTHVPGIYAVQIYIIMOLEK 1620
 1561 KLEGDRLDMNCTLPSPDOVVLVGTBEGLYALNVKNSLTHVPGIYAVQIYIIMOLEK 1620
 1621 LMIAGEERALCLVDYKVKQSLAQSHLPAQPDISPNIPEAVNGCHLFGAGKILENGLCICA 1680
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 1681 AMPSKVILIRYENENTSKYCIKRIEITSEPCSCIHFTNYSILIGTNKFEYIDMKQYTLLEF 1740
 1681 AMPSKVILIRYENENTSKYCIKRIEITSEPCSCIHFTNYSILIGTNKFEYIDMKQYTLLEF 1740
 1741 LDKNDHSLAPAVFAASSNFVSIYVNSAGOREEYLLCFHEFGVIVUSYGRSRSTDOLK 1800
 1741 LDKNDHSLAPAVFAASSNFVSIYVNSAGOREEYLLCFHEFGVIVUSYGRSRSTDOLK 1800
 1801 WSRPLAFAYREPYLVTHFNLELEYIEIQARSASAGTPARAYLIDINPRYLGPAISSGAY 1860
 1801 WSRPLAFAYREPYLVTHFNLELEYIEIQARSASAGTPARAYLIDINPRYLGPAISSGAY 1860
 1861 IASSYQDKLRVICCKGNLVKESGTEHHRGPSTSRSSPNKRGPTYNEHITKXVASSPAP 1920
 1861 IASSYQDKLRVICCKGNLVKESGTEHHRGPSTSRSSPNKRGPTYNEHITKXVASSPAP 1920
 1921 EGPSPHREPESTHRRYREGTELRDQKSGRPLERKSGRMJLSTREBSRGLFEDSSSG 1980
 1921 EGPSPHREPESTHRRYREGTELRDQKSGRPLERKSGRMJLSTREBSRGLFEDSSSG 1980
 1981 RLPAGAVRTPLESQVKKGQASQVFTVTVYVYMNKKLDLPLAMSVLARIIOANGEIR 2040

Db 1981 RLPAAGVRLPRLSQVNGRGSGASQVFTVNTVTTYDNKKLNLPAWMSVLRITQNGEIR 2040
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Db 2041 QQVEKSVLRDYC 2053

RESULT 3
US-10-757-262-52
Sequence 52, Application US/10757262
Publication No. US20040197825A1
GENERAL INFORMATION:
APPLICANT: Karicheti, Venkateswarlu
APPLICANT: Sijos-Santiago, Imaculada
APPLICANT: Eliasof, Scott D
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
FILE REFERENCE: MP103-007P1RNCNMIM
CURRENT APPLICATION NUMBER: US/10/757,262
CURRENT FILING DATE: 2004-01-14
PRIOR APPLICATION NUMBER: US 60/440,318
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/444,783
PRIOR FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: US 60/457,901
PRIOR FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: US 60/468,775
PRIOR FILING DATE: 2003-05-08
PRIOR APPLICATION NUMBER: US 60/471,614
PRIOR FILING DATE: 2003-05-19
PRIOR APPLICATION NUMBER: US 60/478,742
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: US 60/488,529
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/491,156
PRIOR FILING DATE: 2003-07-30
PRIOR APPLICATION NUMBER: US 60/499,594
PRIOR FILING DATE: 2003-09-02
PRIOR APPLICATION NUMBER: US 60/506,332
PRIOR FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 136
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52
LENGTH: 2053
TYPE: PRT
ORGANISM: Homo sapiens
US-10-757-262-52

Query Match 100.0%; Score 10490; DB 16; Length 2053;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2053; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 181 DLTLNLRYEDQDLNLIQFYLAELILAVSHVHLMGVYHRDIPKPNILIVDRTHIKLVDF 240
QY 241 GSAAKNSNKNVNAKLPIGTPDYNAPEVLTWNAGDGKGYGLDCMWSGVAYEMTIGR 300
Db 241 GSAAKNSNKNVNAKLPIGTPDYNAPEVLTWNAGDGKGYGLDCMWSGVAYEMTIGR 300
QY 301 SPFAEGTSARTFNINIMNFORFLKFPDDPKVSSDFLDLIQSLICQKRLKEGLCHPFF 360
Db 301 SPFAEGTSARTFNINIMNFORFLKFPDDPKVSSDFLDLIQSLICQKRLKEGLCHPFF 360
QY 361 SKIDNNIRNSPPRPVPLTKSDDDTSNDEPKNSWSSPCQSPSGFSGEELPFVGS 420
Db 361 SKIDNNIRNSPPRPVPLTKSDDDTSNDEPKNSWSSPCQSPSGFSGEELPFVGS 420
QY 421 YSKALGILGRSESVSGDSPAKTSMKELLIKSKELQDQDKCHKKEQENTRLHRYVS 480
Db 421 YSKALGILGRSESVSGDSPAKTSMKELLIKSKELQDQDKCHKKEQENTRLHRYVS 480
QY 481 EYEAVLSQYVELKASEFORSLLBODLATYITTECSLSKRSLEQARMEVSOEDKALQLH 540
Db 481 EYEAVLSQYVELKASEFORSLLBODLATYITTECSLSKRSLEQARMEVSOEDKALQLH 540
QY 541 DIREGSRLOIKQGEYQAOYEMRMIMNOLBODLVASRRSDIYESELRESRLAAEFK 600
Db 541 DIREGSRLOIKQGEYQAOYEMRMIMNOLBODLVASRRSDIYESELRESRLAAEFK 600
QY 601 RKATECOHKLKANDOGKPEVEGYAKLEKINAEOQLIOELOEKLKAKARELEKL 660
Db 601 RKATECOHKLKANDOGKPEVEGYAKLEKINAEOQLIOELOEKLKAKARELEKL 660
QY 661 QNRDSSGIRKKUVEAERHSHLENKYKRLETERREBNRLKDIQYKSQOIQQMADKIL 720
Db 661 QNRDSSGIRKKUVEAERHSHLENKYKRLETERREBNRLKDIQYKSQOIQQMADKIL 720
QY 721 ELBEKHRAQVSAOHLBYHLKQKOHYEKKVLDNOIKDOLADKETLENMOMHBEBAH 780
Db 721 ELBEKHRAQVSAOHLBYHLKQKOHYEKKVLDNOIKDOLADKETLENMOMHBEBAH 780
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Db 961 KFDALRNSCTVITDLBEOQLQUTEDNAELNNOFFYSKQDLEASGANDETIVOLRSEVDHL 1020
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 Qy 1381 ERHNNHPIHREFNGLMNRATKCAVCLDTVHFGROASCLCQWCHPKSTCIPATGSLP 1440
 Db 1381 ERHNNHPIHREFNGLMNRATKCAVCLDTVHFGROASCLCQWCHPKSTCIPATGSLP 1440
 Qy 1441 AEYATHTFAFCRDKNKSPGLQTKBPSSSLHLEGMKVPNNKRGQGMGRKXIVLEGSK 1500
 Db 1441 AEYATHTFAFCRDKNKSPGLQTKBPSSSLHLEGMKVPNNKRGQGMGRKXIVLEGSK 1500
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 Db 1501 VLLYDNEARAGORPVEEFELCLPDGVSTHGAVASSELANTAKAEAEADAKLGLNSL 1560
 Qy 1561 KLEGGDRDLDMNCTLPFSDQVVLVGTBERGLYALNVLKSLTHVPGIGAVFOIYIIXDLK 1620
 Db 1561 KLEGGDRDLDMNCTLPFSDQVVLVGTBERGLYALNVLKSLTHVPGIGAVFOIYIIXDLK 1620
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 Db 1621 LMIAGEERALCLVDVKKVKSQSLAQSHLPAQPDISPNIPEAVKGCFLFAGKIEBGLCICA 1680
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 Db 1681 AMPSKVILLYNNELSKYCIKKEIETSEPCSHFTNYSLIGTNKYEIDMKQYTLIEF 1740
 Qy 1741 LDKNDSLAPAVFAASNSFPVSVQVNSAGOREEYLLCFHEGCVFVDSIGRSRTDML 1800
 Db 1741 LDKNDSLAPAVFAASNSFPVSVQVNSAGOREEYLLCFHEGCVFVDSIGRSRTDML 1800
 Qy 1801 WSLPLAFAYREBYLFVTHFNSLEVIEIQARSSAGTPARAYLDIPNRYLGAIPASGAY 1860
 Db 1801 WSLPLAFAYREBYLFVTHFNSLEVIEIQARSSAGTPARAYLDIPNRYLGAIPASGAY 1860
 Qy 1861 LMSYDDKLAVICCKGNLVESGTEHHRGSTRSSSNKGPPTYNHITKRVASGAPP 1920
 Db 1861 LMSYDDKLAVICCKGNLVESGTEHHRGSTRSSSNKGPPTYNHITKRVASGAPP 1920
 Qy 1921 EGSHPREPSTPHRYEGRTLRDKSRRPLREKSPGMLSTRRSPGRPLFEDSSRG 1980
 Db 1921 EGSHPREPSTPHRYEGRTLRDKSRRPLREKSPGMLSTRRSPGRPLFEDSSRG 1980
 Qy 1981 RLPAGAVRTPLSQVNRGQASQVFTVNTVYTYDMNKKLDNLPAMWSVLRITQLNGEIR 2040
 Db 1981 RLPAGAVRTPLSQVNRGQASQVFTVNTVYTYDMNKKLDNLPAMWSVLRITQLNGEIR 2040
 Qy 2041 QOVEKSVLRTDYC 2053
 Db 2041 QOVEKSVLRTDYC 2053
 RESULT 4
 US-10-415-011-21
 ; Sequence 21, Application US/10415011
 ; Publication No. US20040053394A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE CORPORATION
 ; APPLICANT: GURURAJAN, Rajagopal
 ; APPLICANT: BAUGHN, Mariah R.
 ; APPLICANT: CHAMLA, Narinder K.
 ; APPLICANT: ELLIOTT, Vicki S.
 ; APPLICANT: XU, Yuming
 ; APPLICANT: ARVIZU, Chandra S.
 ; APPLICANT: VAO, Montique G.
 ; APPLICANT: RAMKOMAR, Jayalakmi
 ; APPLICANT: DING, Li
 ; APPLICANT: TANG, Y. Tom
 ; APPLICANT: HAFALIA, April J.A.
 ; APPLICANT: NGUYEN, Daniel B.

; APPLICANT: GANDHI, Ameena R.
 ; APPLICANT: LU, Yan
 ; APPLICANT: YUE, Henry
 ; APPLICANT: BURFORD, Neil
 ; APPLICANT: BANDMAN, Olga
 ; APPLICANT: TRIBOULEY, Catherine M.
 ; APPLICANT: LAL, Preeti G.
 ; APPLICANT: RECIPON, Shirley A.
 ; APPLICANT: LU, Dying Aina M.
 ; APPLICANT: BOROWSKI, Mark L.
 ; APPLICANT: THORNTON, Michael B.
 ; APPLICANT: SWARNAKER, Anita
 ; APPLICANT: THANGAVELU, Kavitha
 ; APPLICANT: KHAN, Farrah A.
 ; APPLICANT: ISON, Craig H.
 ; TITLE OF INVENTION: HUMAN KINASES
 ; FILE REFERENCE: PI-0262 USN
 ; CURRENT APPLICATION NUMBER: US/10/415, 011
 ; CURRENT FILING DATE: 2003-04-18
 ; PRIOR APPLICATION NUMBER: PCT/US01/47728
 ; PRIOR FILING DATE: 2001-10-20
 ; PRIOR APPLICATION NUMBER: US 60/242, 410
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: US 60/244, 068
 ; PRIOR FILING DATE: 2000-10-27
 ; PRIOR APPLICATION NUMBER: US 60/245, 708
 ; PRIOR FILING DATE: 2000-11-03
 ; PRIOR APPLICATION NUMBER: US 60/247, 672
 ; PRIOR FILING DATE: 2000-11-09
 ; PRIOR APPLICATION NUMBER: US 60/249, 565
 ; PRIOR FILING DATE: 2000-11-16
 ; PRIOR APPLICATION NUMBER: US 60/252, 730
 ; PRIOR FILING DATE: 2000-11-22
 ; PRIOR APPLICATION NUMBER: US 60/250, 807
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 21
 ; LENGTH: 2054
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20040053394A1 7484498CD1
 US-10-415-011-21
 Query Match 95.6%; Score 10032.5; DB 15; Length 2054;
 Best Local Similarity 95.8%; Pred. No. 0;
 Matches 1981; Conservative 2; Mismatches 4; Indels 81; Gaps 3;
 Qy 1 MLKFKYGANPLDAGABPIASRASHNLFPQKPEPMTQOQWSPLSREGIIDLALFVLE 60
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 Qy 61 ECSOPALMKIKVSNVVRKYSDTIAELOLSASQDFEVRSLVGCDFEAVOVVRKANG 120
 Db 61 ECSOPALMKIKVSNVVRKYSDTIAELOLSASQDFEVRSLVGCDFEAVOVVRKANG 120
 Qy 121 DIYAMKVMKKALLAQEQVSPFEERNNILSRSTSPWIPOLQYAFODKNLILYMEBYOPG 180
 Db 121 DIYAMKVMKKALLAQEQVSPFEERNNILSRSTSPWIPOLQYAFODKNLILYMEBYOPG 180
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 Db 181 DLISLNRVEDQDENLQFYLAELILAVSHVHLNGYVARDIKPENILVDRGHIKLVDP 240
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 Db 241 GSAKKNKSNMKNNAKLPICTPDYMAPEVLTVMNGGSKGYGIDCDMWSGVAYEMTYGR 300
 Qy 301 SPFAEGTSARTFNINNFORFLKFPDDPKVSSDFDLILQSLCQGERLKFGGLCCHPFF 360
 Db 301 SPFAEGTSARTFNINNFORFLKFPDDPKVSSDFDLILQSLCQGERLKFGGLCCHPFF 360

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QY 361 SKIDMNNIRNSPPFPVTLKSDDDTSNPDPEKNSWSSPCOLSPSGSGEELPVGVS 420
Db 361 SKIDMNNIRNSPPFPVTLKSDDDTSNPDPEKNSWSSPCOLSPSGSGEELPVGVS 420
QY 421 YSKALGILGRSESVGLDSPAKTSSMEKKLLIKSELQDSQDKHMEQEMTRLRHVS 480
Db 421 YSKALGILGRSESVGLDSPAKTSSMEKKLLIKSELQDSQDKHMEQEMTRLRHVS 480
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Db 481 EYEAVALSOKVEIKASETQSRSLLEODLATYITECSSLKSLSEQARMEVSGEEDKALQJLH 540
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Db 541 DIREQSRKLOEIKEQEYQAOVEEMRLMMNQLEEDVSARRSDLYSESLRESRLAEERK 600
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Db 661 NTRQAKERARELEKQONREDSSEGRKULVEAEERHSLKVKRLFTMERENMLKOD 720
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Db 1005 GANDEIYOLRSEVDHARREITEREMQUTSOKQOTMALKTTCMLSEOWMDLEALNDELLE 1064
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Db 1081 KERQWEAMRSVLDGKESQPECHVRELQOMLDEKOSRARADQRTESQOVVELAVKEHKA 1140
QY 1125 ETLALQALKEQKLAESLSDPKLANDLEKKHMLJENNAASLQOKLETETELKQRLLEEQAK 1184
Db 1125 ETLALQALKEQKLAESLSDPKLANDLEKKHMLJENNAASLQOKLETETELKQRLLEEQAK 1184
QY 1141 ETLALQALKEQKLAESLSDPKLANDLEKKHMLJENNAASLQOKLETETELKQRLLEEQAK 1200
Db 1141 ETLALQALKEQKLAESLSDPKLANDLEKKHMLJENNAASLQOKLETETELKQRLLEEQAK 1200
QY 1185 LQQQMDLQKNHIFRLTOGLOEALDRADLLKTERSPDLEQOLENIOVLVYSHHEKVMGTSISQ 1244
Db 1185 LQQQMDLQKNHIFRLTOGLOEALDRADLLKTERSPDLEQOLENIOVLVYSHHEKVMGTSISQ 1244
QY 1201 LQQQMDLQKNHIFRLTOGLOEALDRADLLKTERSPDLEQOLENIOVLVYSHHEKVMGTSISQ 1260
Db 1201 LQQQMDLQKNHIFRLTOGLOEALDRADLLKTERSPDLEQOLENIOVLVYSHHEKVMGTSISQ 1260
QY 1245 QTKLIDPLQAMQDPAKKKKGLFSRRKEDPALPTQVPLQVNELKLALEKAKACALEEBA 1304
Db 1245 QTKLIDPLQAMQDPAKKKKGLFSRRKEDPALPTQVPLQVNELKLALEKAKACALEEBA 1304
QY 1261 QTKLIDPLQAMQDPAKKKKGLFSRRKEDPALPTQVPLQVNELKLALEKAKACALEEBA 1305
Db 1261 QTKLIDPLQAMQDPAKKKKGLFSRRKEDPALPTQVPLQVNELKLALEKAKACALEEBA 1305
QY 1305 LOKTRIEIERSAREEAARAKADHDPSTPATRQOIASAIYRSEPHQPSAMSLIAPPSS 1364
Db 1305 LOKTRIEIERSAREEAARAKADHDPSTPATRQOIASAIYRSEPHQPSAMSLIAPPSS 1364
QY 1306 LOKTRIEIERSAREEAARAKADHDPSTPATRQOIASAIYRSEPHQPSAMSLIAPPSS 1365
Db 1306 LOKTRIEIERSAREEAARAKADHDPSTPATRQOIASAIYRSEPHQPSAMSLIAPPSS 1365
QY 1365 RRKESSTPEEFSRRLKERMHNNIPIRRFNVGLNMRATKAVCLDPTHFERQASKLECOVM 1424
Db 1365 RRKESSTPEEFSRRLKERMHNNIPIRRFNVGLNMRATKAVCLDPTHFERQASKLECOVM 1424
QY 1366 RRKESSTPEEFSRRLKERMHNNIPIRRFNVGLNMRATKAVCLDPTHFERQASKLECOVM 1425
Db 1366 RRKESSTPEEFSRRLKERMHNNIPIRRFNVGLNMRATKAVCLDPTHFERQASKLECOVM 1425

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QY 1425 CHPKCSTCLPATCGIPAEYAHTHTEAFCDKDKNSPGLQTKERSSSLHJEGMKVPRNNKR 1484
Db 1425 CHPKCSTCLPATCGIPAEYAHTHTEAFCDKDKNSPGLQTKERSSSLHJEGMKVPRNNKR 1485
QY 1485 GOQWMDRKTYVLEGSKVLTYDNEAREAGORPVEEPELCLPDQDVSITHGAVGASELANAK 1544
Db 1485 GOQWMDRKTYVLEGSKVLTYDNEAREAGORPVEEPELCLPDQDVSITHGAVGASELANAK 1545
QY 1545 A-----EKAADAKL 1554
Db 1545 ADVPIYIKMESHPTTWPGRITLYLLAPSPDQKRWYALLESVAGVRSEKADADAKL 1605
QY 1555 LGSNLKLEGGDRLLMNCCTLPSPDOVTVGTEEGYALANTLKNLTHYPIGAVQIYI 1614
Db 1555 LGSNLKLEGGDRLLMNCCTLPSPDOVTVGTEEGYALANTLKNLTHYPIGAVQIYI 1614
QY 1606 LGSNLKLEGGDRLLMNCCTLPSPDOVTVGTEEGYALANTLKNLTHYPIGAVQIYI 1665
Db 1606 LGSNLKLEGGDRLLMNCCTLPSPDOVTVGTEEGYALANTLKNLTHYPIGAVQIYI 1665
QY 1615 KDLKELMIAGEERALCLVDYKVKVQSLAQSHLPAQPDISPNIPEAVGCHLFGAGKLEN 1674
Db 1615 KDLKELMIAGEERALCLVDYKVKVQSLAQSHLPAQPDISPNIPEAVGCHLFGAGKLEN 1675
QY 1666 KDLKELMIAGEERALCLVDYKVKVQSLAQSHLPAQPDISPNIPEAVGCHLFGAGKLEN 1725
Db 1666 KDLKELMIAGEERALCLVDYKVKVQSLAQSHLPAQPDISPNIPEAVGCHLFGAGKLEN 1725
QY 1675 GLCTIAMPSPKVIILRYNENISKYCIKRIETSEPCSIHFTNYSILIGTNKFEYIDMKQ 1734
Db 1675 GLCTIAMPSPKVIILRYNENISKYCIKRIETSEPCSIHFTNYSILIGTNKFEYIDMKQ 1785
QY 1726 GLCTIAMPSPKVIILRYNENISKYCIKRIETSEPCSIHFTNYSILIGTNKFEYIDMKQ 1785
Db 1726 GLCTIAMPSPKVIILRYNENISKYCIKRIETSEPCSIHFTNYSILIGTNKFEYIDMKQ 1785
QY 1735 YLLEEFLLKNDHSLAPAVFAASNSFPVSIYOUNSAGCREBYLLCFHEFGVFDVSYGRS 1794
Db 1735 YLLEEFLLKNDHSLAPAVFAASNSFPVSIYOUNSAGCREBYLLCFHEFGVFDVSYGRS 1845
QY 1795 RTDDLKMSRLPLAFYREBYLVFTHFNLSLEVTEIOARSASCTPARAYLIDINPRLTGPAT 1854
Db 1795 RTDDLKMSRLPLAFYREBYLVFTHFNLSLEVTEIOARSASCTPARAYLIDINPRLTGPAT 1905
QY 1846 RTDDLKMSRLPLAFYREBYLVFTHFNLSLEVTEIOARSASCTPARAYLIDINPRLTGPAT 1905
Db 1846 RTDDLKMSRLPLAFYREBYLVFTHFNLSLEVTEIOARSASCTPARAYLIDINPRLTGPAT 1905
QY 1855 SSGAIIYLAASYODKLRVYCKGNTVKESGTEHHRGPSTSRSPNKGCPPTYNEHITKRYA 1914
Db 1855 SSGAIIYLAASYODKLRVYCKGNTVKESGTEHHRGPSTSRSPNKGCPPTYNEHITKRYA 1965
QY 1906 SSGAIIYLAASYODKLRVYCKGNTVKESGTEHHRGPSTSRSPNKGCPPTYNEHITKRYA 1965
Db 1906 SSGAIIYLAASYODKLRVYCKGNTVKESGTEHHRGPSTSRSPNKGCPPTYNEHITKRYA 1965
QY 1915 SSPAPBEGSPHREPSPTPHRREGRTLEBRDPSGRPLERKSPGRLMSTREBSPGLF 1974
Db 1915 SSPAPBEGSPHREPSPTPHRREGRTLEBRDPSGRPLERKSPGRLMSTREBSPGLF 1974
QY 1966 SSPAPBEGSPHREPSPTPHRREGRTLEBRDPSGRPLERKSPGRLMSTREBSPGLF 2025
Db 1966 SSPAPBEGSPHREPSPTPHRREGRTLEBRDPSGRPLERKSPGRLMSTREBSPGLF 2025
QY 1975 EDSSRGRLPAGAVRTPLSQVVKGRGQSA 2002
Db 1975 EDSSRGRLPAGAVRTPLSQVVKGRGQSA 2002
QY 2026 EDSSRGRLPAGAVRTPLSQVVKWMDQSS 2053
Db 2026 EDSSRGRLPAGAVRTPLSQVVKWMDQSS 2053

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RESULT 5
 US-10-028-946-2
 ; Sequence 2, Application US/10028946
 ; Publication No. US20020123622A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yu, Xuanhuan
 ; APPLICANT: Miranda, Maricar
 ; TITLE OF INVENTION: No. US20020123622A1 Human Kinases and Polynucleotides Encoding
 ; FILE REFERENCE: Lex-0289-USA
 ; CURRENT APPLICATION NUMBER: US/10/028,946
 ; PRIOR FILING DATE: 2001-12-20
 ; PRIOR APPLICATION NUMBER: US 60/258,335
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 2054
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-028-946-2

Query Match 95.5%; Score 10022.5; DB 13; Length 2054;
 Best Local Similarity 95.7%; Pred. No. 0;
 Matches 1979; Conservative 3; Mismatches 5; Indels 81; Gaps 3;

1 MLKRYGARNPLDGAABPIASRASRLNLFQGGKPPMTQOQMSPLSREGILDALFVLF 60
 |||||

Db 1 MLFFKYGABNPLDGAAPLAPASRSLNLFQGGKPPFMTQQQMSPLSREGILDALFVLF 60
 QY 61 EESOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDPEVRSIVGCGHPAEVQVVRKAC 120
 Db 61 EESOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDPEVRSIVGCGHPAEVQVVRKAC 120
 QY 121 DIYAMKVMKKALLAOEVSFFEEERNILSRSTSPMIPOLQVAFODKNNHYLMEEPG 180
 Db 121 DIYAMKVMKKALLAOEVSFFEEERNILSRSTSPMIPOLQVAFODKNNHYLMEEPG 180
 QY 181 DLISLNRBYEDQDENLQFYLAELLAVHSVHLMGVHNDIKENILVDRTHIKLVDF 240
 Db 181 DLISLNRBYEDQDENLQFYLAELLAVHSVHLMGVHNDIKENILVDRTHIKLVDF 240
 QY 241 GSAKKNKSNKVNAPKPIGTDPYMAPEVLTVMNGDGKTYGLDCDMWSGVINAYEM1YGR 300
 Db 241 GSAKKNKSNKVNAPKPIGTDPYMAPEVLTVMNGDGKTYGLDCDMWSGVINAYEM1YGR 300
 QY 301 SPPAEGTSARTFNINNFORFLKFPDDPKVSDFLDLOSILCGOKERLKFEGLCCHPFF 360
 Db 301 SPPAEGTSARTFNINNFORFLKFPDDPKVSDFLDLOSILCGOKERLKFEGLCCHPFF 360
 QY 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNPFDEPKNSVWSSPCQLSPSGSGEELPFVGS 420
 Db 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNPFDEPKNSVWSSPCQLSPSGSGEELPFVGS 420
 QY 421 YSKALDILGRSBSVGLDSPATSSMEKKL1KSELQDSQDKCHMOEMTRLHRYS 480
 Db 421 YSKALDILGRSBSVGLDSPATSSMEKKL1KSELQDSQDKCHMOEMTRLHRYS 480
 QY 481 EYFAVLVSOKEVELKASETORSLLEODLATYITECSSLKSLBOARHVSQEDKALQHL 540
 Db 481 EYFAVLVSOKEVELKASETORSLLEODLATYITECSSLKSLBOARHVSQEDKALQHL 540
 QY 541 DI1REGSRKLOEIKEGYQAOVEEMRLMMNQLEEDLVASARRSDLYESELRESRLAEBK 600
 Db 541 DI1REGSRKLOEIKEGYQAOVEEMRLMMNQLEEDLVASARRSDLYESELRESRLAEBK 600
 QY 601 RKAATEQHLKAKOGKPEVGYATLEKINAEQOLKIOELQKLEKA----- 648
 Db 601 RKAATEQHLKAKOGKPEVGYATLEKINAEQOLKIOELQKLEKA----- 648
 QY 649 -----AKERARELEKQNRDESSSEGRKXVLVEABERHSLNNVKKLETMERENRXLKD 704
 Db 649 -----AKERARELEKQNRDESSSEGRKXVLVEABERHSLNNVKKLETMERENRXLKD 704
 QY 705 IOTKSQOIQOMADKILELEBKREAOVSAQHLVHLKOKOHYBEKIKVLDNQIKKDLAD 764
 Db 705 IOTKSQOIQOMADKILELEBKREAOVSAQHLVHLKOKOHYBEKIKVLDNQIKKDLAD 764
 QY 765 KETLEMMQORHEBEAHEKGI1SEQAMINANDSKIRSLBORIVELSEANKLAANS1LT 824
 Db 765 KETLEMMQORHEBEAHEKGI1SEQAMINANDSKIRSLBORIVELSEANKLAANS1LT 824
 QY 825 OBNMKAQOEMISELRQOKFYLETQAGKLEAONRKLEBOLEKISHOHSQNNRLLLEETL 884
 Db 825 OBNMKAQOEMISELRQOKFYLETQAGKLEAONRKLEBOLEKISHOHSQNNRLLLEETL 884
 QY 885 REVSLNEHQKLEKQKLTQLSIQERESQULTAQARAALSESQURQAKTELEETTA 944
 Db 885 REVSLNEHQKLEKQKLTQLSIQERESQULTAQARAALSESQURQAKTELEETTA 944
 QY 945 EBEIQALTNRDEIQKFPALNSCTVITDLBEQNLQLTEDNAELNANNFYLSKQDEAS 1004
 Db 945 EBEIQALTNRDEIQKFPALNSCTVITDLBEQNLQLTEDNAELNANNFYLSKQDEAS 1004
 QY 1005 GANDEIVQARSEVDHLRRSITREMOQTSOKOTMEALKTTCTMLLEQWMDLALNDELLE 1064
 Db 1005 GANDEIVQARSEVDHLRRSITREMOQTSOKOTMEALKTTCTMLLEQWMDLALNDELLE 1064
 QY 1065 KERQWEAMRSVLDGDEKSQECRVRLEQMLDTEKOSRABADQRTESRQVVELAVENKA 1124
 Db 1065 KERQWEAMRSVLDGDEKSQECRVRLEQMLDTEKOSRABADQRTESRQVVELAVENKA 1124
 QY 1081 KERQWEAMRSVLDGDEKSQECRVRLEQMLDTEKOSRABADQRTESRQVVELAVENKA 1140
 Db 1081 KERQWEAMRSVLDGDEKSQECRVRLEQMLDTEKOSRABADQRTESRQVVELAVENKA 1140

QY 1125 ETLALQALKEOKLKAESLSDKLNDELKKGAMLEMMABSLQOKLETRETELKORLLEBOAK 1184
 Db 1141 ETLALQALKEOKLKAESLSDKLNDELKKGAMLEMMABSLQOKLETRETELKORLLEBOAK 1200
 QY 1185 LQOQMDQKNNHIFRLTOGLQOALDRADLLKTERSDLEYOLENIQVLYSHEKYMESTISO 1244
 Db 1201 LQOQMDQKNNHIFRLTOGLQOALDRADLLKTERSDLEYOLENIQVLYSHEKYMESTISO 1260
 QY 1245 QTKLIDFLQAKNDOPAKKKKGLFSRRKEDPALPTQVPLQYNEKLALBEXKARCALBEA 1304
 Db 1261 QTKLIDFLQAKNDOPAKKKKGLFSRRKEDPALPTQVPLQYNEKLALBEXKARCALBEA 1305
 QY 1305 LOKTRTELSAREBAHRKATDHPHSTPATARQOQAMSAIVRSPEHOSAMSILAPSS 1364
 Db 1306 LOKTRTELSAREBAHRKATDHPHSTPATARQOQAMSAIVRSPEHOSAMSILAPSS 1365
 QY 1365 RRKESSTPEFSRRRLKERHNNH1PHRFNVGLNMRATKCAVCLDTHVHFGQASKLECOVM 1424
 Db 1366 RRKESSTPEFSRRRLKERHNNH1PHRFNVGLNMRATKCAVCLDTHVHFGQASKLECOVM 1425
 QY 1425 CHPKSCTCLPATCGLPABEYATHTFEAFCDKXNSPGLQTKPESSSLHLEGMKVPANNR 1484
 Db 1426 CHPKSCTCLPATCGLPABEYATHTFEAFCDKXNSPGLQTKPESSSLHLEGMKVPANNR 1485
 QY 1485 GQOGMDRKTYVLEGSVULYDNEAREAGORPYEBEELCLPDGDVSTHGAASLANTAK 1544
 Db 1486 GQOGMDRKTYVLEGSVULYDNEAREAGORPYEBEELCLPDGDVSTHGAASLANTAK 1545
 QY 1545 A-----EKAEDAKL 1554
 Db 1546 ADVPYLKRSHSPHTTCWGRGLTYLLABSPDKQKWMTLBSVAGRVSRKAEADAL 1605
 QY 1555 LGNSLLKLEGGDRDLNMCCTLPESDQVVLVGTTEGLYALNVLKNSLTHVPGIGAVFOIY11 1614
 Db 1606 LGNSLLKLEGGDRDLNMCCTLPESDQVVLVGTTEGLYALNVLKNSLTHVPGIGAVFOIY11 1665
 QY 1615 KOLEKLM1AGEBRALCLVDVKKVQVQSLAQSHLPAPQD1SPN1FEAVKCHLFGAGK1EN 1674
 Db 1666 KOLEKLM1AGEBRALCLVDVKKVQVQSLAQSHLPAPQD1SPN1FEAVKCHLFGAGK1EN 1725
 QY 1675 GLCICAMPKSVI1RYNENLSKYCIRKEIETSEPCSC1HFNYSILGTNKFYEIDMKO 1734
 Db 1726 GLCICAMPKSVI1RYNENLSKYCIRKEIETSEPCSC1HFNYSILGTNKFYEIDMKO 1785
 QY 1735 YTLBEFLDKNDHSLAPVFAASSNSFPVSIQVNSAGOREEYLLCFHEGVFVDSYGRS 1794
 Db 1786 YTLBEFLDKNDHSLAPVFAASSNSFPVSIQVNSAGOREEYLLCFHEGVFVDSYGRS 1845
 QY 1795 RTDDLKMSRLPLAFAYREBYLFTVTHNSLEVE1EIQARSSAGTPAAYLD1PNPRYLGP1 1854
 Db 1846 RTDDLKMSRLPLAFAYREBYLFTVTHNSLEVE1EIQARSSAGTPAAYLD1PNPRYLGP1 1905
 QY 1855 SSGATY1LASSYODK1RV1CCGNLVKESGTEHHRGPTSRSSPNKRGPTTYNHEHTKVA 1914
 Db 1906 SSGATY1LASSYODK1RV1CCGNLVKESGTEHHRGPTSRSSPNKRGPTTYNHEHTKVA 1965
 QY 1915 SSPAPPEGSHPREBTPHRYREGRTELNRDQSPGRPLEREXSPGRMLSTRERESGRL 1974
 Db 1966 SSPAPPEGSHPREBTPHRYREGRTELNRDQSPGRPLEREXSPGRMLSTRERESGRL 2025
 QY 1975 EDSRGRPLPAGAVRTP1LQVKKRGOSA 2002
 Db 2026 EDSRGRPLPAGAVRTP1LQVKKRGOSA 2053

RESULT 6

US-10-618-941-67
 ; Sequence 67, Application US/10618941
 ; Publication No. US2004019792A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WHYTE, DAVID
 ; APPLICANT: MANNING, GERARD

```

; APPLICANT: CAENEPEEL, SEAN
; TITLE OF INVENTION: NOVEL KINASES
; FILE REFERENCE: 034536-0321
; CURRENT APPLICATION NUMBER: US/10/618,941
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/395,632
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 67
; LENGTH: 2055
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-618-941-67

Query Match      95.4%; Score 10011; DB 16; Length 2055;
Best Local Similarity 95.7%; Pred. No. 0;
Matches 1979; Conservative 3; Mismatches 5; Indels 82; Gaps 4;

QY      1 MLKFKTGANNPLDAGAAEPPLASASRLNLPFGCKPFPMTQQOMSPLSREGTLDALFVLFE 60
DB      1 MLKFKTGANNPLDAGAAEPPLASASRLNLPFGCKPFPMTQQOMSPLSREGTLDALFVLFE 60
QY      61 ECGOPALMKIKHVSNFVRK-YSDPTIAELOLOPSAKDFEVSIVGCGHFAEYQVVEKAT 119
DB      61 ECGOPALMKIKHVSNFVEVYSDPTIAELOLOPSAKDFEVSIVGCGHFAEYQVVEKAT 120
QY      120 GDIYANKVKKKALLAQEOVSFPEEERNILSRSTSPWITPOLQYAFODKNHLYIMEEYQPG 179
DB      121 GDIYANKVKKKALLAQEOVSFPEEERNILSRSTSPWITPOLQYAFODKNHLYIMEEYQPG 180
QY      180 GDLSILNRYEODLNLQFYLAELILAVSHVLMGYVHRDIKPNITLVDRIGHIKLVLD 239
DB      181 GDLSILNRYEODLNLQFYLAELILAVSHVLMGYVHRDIKPNITLVDRIGHIKLVLD 240
QY      240 FGSAAIKNSKYNNAKLPIGTPDYMAPEVLTVMNGDGKGYGLDCDMSVGVYIAYEMIVG 299
DB      241 FGSAAIKNSKYNNAKLPIGTPDYMAPEVLTVMNGDGKGYGLDCDMSVGVYIAYEMIVG 300
QY      300 RSPFAGTSARTYNNINMFORPLKFPDDPKVSSDFDLIOSLLCGQEKRLKFPGLCCHP 359
DB      301 RSPFAGTSARTYNNINMFORPLKFPDDPKVSSDFDLIOSLLCGQEKRLKFPGLCCHP 360
QY      360 FSKIDMNNINRSPFPVPTKSDDDTSNPDEPKNSWSSPCQLSPSGSGEELFPVPG 419
DB      361 FSKIDMNNINRSPFPVPTKSDDDTSNPDEPKNSWSSPCQLSPSGSGEELFPVPG 420
QY      420 SYSKALGILGRSESVVSGLDSPAKTSMKKLLIKSKELODSQDKCHMEQEMTRLHRRY 479
DB      421 SYSKALGILGRSESVVSGLDSPAKTSMKKLLIKSKELODSQDKCHMEQEMTRLHRRY 480
QY      480 SEVEAYLSQKEVELKASETORSLLEODLAYITTECSLKRSLEQAMNVSQEDDKALQLL 539
DB      481 SEVEAYLSQKEVELKASETORSLLEODLAYITTECSLKRSLEQAMNVSQEDDKALQLL 540
QY      540 HDIREOSRKQOEIKEOYQAVEEMRLMMNQLEEDIVASARRSDLYESELRREGSLAAEF 599
DB      541 HDIREOSRKQOEIKEOYQAVEEMRLMMNQLEEDIVASARRSDLYESELRREGSLAAEF 600
QY      600 KRKATBCQHLAKADQKPEVEYAKLEKINAEOQLIQELOEKLKA----- 648
DB      601 KRKATBCQHLAKADQKPEVEYAKLEKINAEOQLIQELOEKLKA----- 660
QY      649 -----AKERAPRELKQNRDESGEGRKLVAEAPRRSHLENKYRLTMEERREARLKD 703
DB      661 QNIRQAERERARELEKQNRDESGEGRKLVAEAPRRSHLENKYRLTMEERREARLKD 720
QY      704 DIOTKSQOIQOMADKILELEKREAOVSAQHLVHLKQKOEYEEKIKVLDNQIKKDLA 763
DB      721 DIOTKSQOIQOMADKILELEKREAOVSAQHLVHLKQKOEYEEKIKVLDNQIKKDLA 780
QY      764 DKETLENNQPHHEEAHEKGIISQKAMINAMDSKIRSLERQIVELSEANKLAANSLF 823
DB      764 DKETLENNQPHHEEAHEKGIISQKAMINAMDSKIRSLERQIVELSEANKLAANSLF 823
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DB      781 DKETLENNQPHHEEAHEKGIISQKAMINAMDSKIRSLERQIVELSEANKLAANSLF 840
QY      824 TORNNKAOEEMISETROOKFYLETOAGKLEPAQNKLEBOLEKISHQHSNDKNRILLEETR 883
DB      841 TORNNKAOEEMISETROOKFYLETOAGKLEPAQNKLEBOLEKISHQHSNDKNRILLEETR 900
QY      884 LREYSLHEBOKELEKROLTELQSLQERESQTLAQARALLESQROAKTELEETTAE 943
DB      901 LREYSLHEBOKELEKROLTELQSLQERESQTLAQARALLESQROAKTELEETTAE 960
QY      944 ABEELQALTARDEIQRFKDALRNSCTVITDLEBQNLQTEDNABLNQNFYLSKQDEA 1003
DB      961 ABEELQALTARDEIQRFKDALRNSCTVITDLEBQNLQTEDNABLNQNFYLSKQDEA 1020
QY      1004 SGANDEIYQLASEVDHLRREITTEEMOULTSQOMELAKTCTMLEBOVMLEALNDEL 1063
DB      1021 SGANDEIYQLASEVDHLRREITTEEMOULTSQOMELAKTCTMLEBOVMLEALNDEL 1080
QY      1064 EKEROMEAMRSVLDGKQFECRVARELORMIDTEKOSPARADORTTESRQVVELAVKEM 1123
DB      1081 EKEROMEAMRSVLDGKQFECRVARELORMIDTEKOSPARADORTTESRQVVELAVKEM 1140
QY      1124 AEIIALQALKEBQIKABESLSDKNDLEKKAMLEBNARSIOQKLETERELKORLLEQA 1183
DB      1141 AEIIALQALKEBQIKABESLSDKNDLEKKAMLEBNARSIOQKLETERELKORLLEQA 1200
QY      1184 KLQOQMDIQKNHIFPLTQGLQALDRADLTLTERSDELYOLENIQVLSHEKVKMEGTIS 1243
DB      1201 KLQOQMDIQKNHIFPLTQGLQALDRADLTLTERSDELYOLENIQVLSHEKVKMEGTIS 1260
QY      1244 QOTKLIDFLQAKMDPAKKKKGLPSRRKEDBALPTQVLEQYNELEKALEKKEKARCALEE 1303
DB      1261 QOTKLIDFLQAKMDPAKKKK-----VLEQYNELEKALEKKEKARCALEE 1305
QY      1304 ALQKTRIELRSAREBAARKATDHPSTPATRQIMSAIYVSPHEOPASMLAPPS 1363
DB      1306 ALQKTRIELRSAREBAARKATDHPSTPATRQIMSAIYVSPHEOPASMLAPPS 1365
QY      1364 SRRKESSTPEEFSRRLKERMHNIIPHRPNVGLNBRATKCAVCLDVFHGRQASKLECOV 1423
DB      1366 SRRKESSTPEEFSRRLKERMHNIIPHRPNVGLNBRATKCAVCLDVFHGRQASKLECOV 1425
QY      1424 MCHPKCSTCLPATCGLPAEVATHTFEAFCRDKMSPSGLQYKPPSSLHLBGMKYPRNNK 1483
DB      1426 MCHPKCSTCLPATCGLPAEVATHTFEAFCRDKMSPSGLQYKPPSSLHLBGMKYPRNNK 1485
QY      1484 RQOQGMDRKYIYLBSSKYLIDNEAREAGQRPVEFEELCLPDGDVSIHGAVGASLEANTYA 1543
DB      1486 RQOQGMDRKYIYLBSSKYLIDNEAREAGQRPVEFEELCLPDGDVSIHGAVGASLEANTYA 1545
QY      1544 KA-----EKAADAK 1553
DB      1546 KADVPIYILKMHSHPTTCMPGRTLYLLAPFPDKQWVTALLESVVAAGRVSEKABADAK 1605
QY      1554 ILGNSILKLEGGDRIDMNCCTLPESDQVVLVGTBEGLYALNVLKNSLTHVPGIGAVFOIYI 1613
DB      1606 ILGNSILKLEGGDRIDMNCCTLPESDQVVLVGTBEGLYALNVLKNSLTHVPGIGAVFOIYI 1665
QY      1614 IYDLKELMIAGEERBALCIVDKYKXKSLAOSHLPAPDISPNIPEAVNGCHLPFGAGKLE 1673
DB      1666 IYDLKELMIAGEERBALCIVDKYKXKSLAOSHLPAPDISPNIPEAVNGCHLPFGAGKLE 1725
QY      1674 NGLCICAMPSPKVVILIRYVENLSKYCIRKELTSPSCSIRHTNYSILIGTNKFEYIDMK 1733
DB      1726 NGLCICAMPSPKVVILIRYVENLSKYCIRKELTSPSCSIRHTNYSILIGTNKFEYIDMK 1785
QY      1734 QYTLLEFLDKNDHSLAPAVFAASNSFPVSIYQVNSAGOREEYLLCFHFPGIFUNSYGR 1793
DB      1786 QYTLLEFLDKNDHSLAPAVFAASNSFPVSIYQVNSAGOREEYLLCFHFPGIFUNSYGR 1845
QY      1794 SRTDILKMSRLPLAFVREPYLFVTHFNSLEVIETIOARSAGTPARAYLDINPPLYLGA 1853
DB      1846 SRTDILKMSRLPLAFVREPYLFVTHFNSLEVIETIOARSAGTPARAYLDINPPLYLGA 1905
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QY 1854 ISSGAITYLASSYQDKLRVYCKGNLYKESGTEHHRGPTSRSSPNKRGPTTNEHTTKRV 1913
DB 1906 ISSGALYALSSYQDKLRVYCKGNLYKESGTEHHRGPTSRSSPNKRGPTTNEHTTKRV 1965
QY 1914 ASSPAPPEGSPHREPTPHRREGRTELRDRKSPGRPLERESPGRMSTRERSPGRU 1973
DB 1966 ASSPAPPEGSPHREPTPHRREGRTELRDRKSPGRPLERESPGRMSTRERSPGRU 2025
QY 1974 FEDSSRGRLPAGAVRTPLSQVKNKGRQSA 2002
DB 2026 FEDSSRGRLPAGAVRTPLSQVKNKWPQSS 2054

RESULT 7
US-09-964-956-9
Sequence 9, Application US/09964956
Publication No. US20040043926A1
GENERAL INFORMATION:
APPLICANT: Gerlach, Valerie L.
APPLICANT: MacDougall, John R.
APPLICANT: Smithson, Glenda
APPLICANT: Millet, Isabelle
APPLICANT: Stone, David
APPLICANT: Gunther, Erik
APPLICANT: Ellerman, Karen
APPLICANT: Grose, William M.
APPLICANT: Alsbrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Burgess, Catherine B.
APPLICANT: Padigaru, Muralidhara
APPLICANT: Kekuda, Ramesh
APPLICANT: Spytek, Kimberly A.
APPLICANT: Leach, Martin D.
APPLICANT: Shimets, Richard A.
TITLE OF INVENTION: No. US20040043926A1el Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-124
CURRENT APPLICATION NUMBER: US/09/964, 956
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/235, 631
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/235, 633
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/235, 808
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236, 064
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236, 065
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236, 066
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236, 135
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/237, 434
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/238, 321
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/238, 399
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/238, 396
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/276, 667
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/294, 823
PRIOR FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 60/304, 868
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 127
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 9
LENGTH: 2066
TYPE: PR
ORGANISM: Homo sapiens

Handwritten: 21402-124
No v 30

US-09-964-956-9
Query Match 95.4%; Score 10007; DB 11; Length 2066;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1979; Conservative 3; Mismatches 7; Indels 82; Gaps 4;
QY 1 MUKFYGANPLDAGAAEPPIASRRLNLFQKGPPEPTQOQMSPLREGIIDLFLVPE 60
DB 1 MUKFYGANPLDAGAAEPPIASRRLNLFQKGPPEPTQOQMSPLREGIIDLFLVPE 60
QY 61 ECSQPALMKIKHVSFNFKYSDPTIAELOPSADFEVRSIVGCGFAVQVVEKATG 120
DB 61 ECSQPALMKIKHVSFNFKYSDPTIAELOPSADFEVRSIVGCGFAVQVVEKATG 120
QY 121 DIYAMKVMKKALLAOEYVSPFEERNTLSNSTSWIIPOLQYAFODKXHLVMEYQPG 180
DB 121 DIYAMKVMKKALLAOEYVSPFEERNTLSNSTSWIIPOLQYAFODKXHLVMEYQPG 180
QY 181 DLSLNRREDOJDNLIQFYLAELILAVSHVLMGVYHRDIKPSNILLVDRGHIKLVDF 240
DB 181 DLSLNRREDOJDNLIQFYLAELILAVSHVLMGVYHRDIKPSNILLVDRGHIKLVDF 240
QY 241 GSAATKNSKVNNAKLPITGPDYMAPEVLTWNAGDKGTGGCDMWSGVIAVEMTYGR 300
DB 241 GSAATKNSKVNNAKLPITGPDYMAPEVLTWNAGDKGTGGCDMWSGVIAVEMTYGR 300
QY 301 SPFAEGTSARTTNNTMNFORFLKPPDDPKVSDFLDIQSLICGQERLKEFGLCCHPF 360
DB 301 SPFAEGTSARTTNNTMNFORFLKPPDDPKVSDFLDIQSLICGQERLKEFGLCCHPF 360
QY 360 SKIDNNNIRNSPPVPVPTLKSDDDTSNDEPKNSWSSPCQLSPSGSGEELPEVGS 420
DB 360 SKIDNNNIRNSPPVPVPTLKSDDDTSNDEPKNSWSSPCQLSPSGSGEELPEVGS 420
QY 421 YSKALGIIGRSBSVSGLDSPAKTSMEKULIKSEKLODSQDKCHKMEQETRLHRRVS 480
DB 421 YSKALGIIGRSBSVSGLDSPAKTSMEKULIKSEKLODSQDKCHKMEQETRLHRRVS 480
QY 480 EVEAVLSQKEVELKASETORSLIEDLATYITECSSLRSLQAMMEVSOEDKALQLH 539
DB 480 EVEAVLSQKEVELKASETORSLIEDLATYITECSSLRSLQAMMEVSOEDKALQLH 539
QY 541 DIREOSRKLQETKEBOYAQVEMRLMNOLEEDIVSARRSDLYESELRESRLAAEBK 600
DB 541 DIREOSRKLQETKEBOYAQVEMRLMNOLEEDIVSARRSDLYESELRESRLAAEBK 600
QY 590 DIREOSRKLQETKEBOYAQVEMRLMNOLEEDIVSARRSDLYESELRESRLAAEBK 599
DB 590 DIREOSRKLQETKEBOYAQVEMRLMNOLEEDIVSARRSDLYESELRESRLAAEBK 599
QY 601 RKATECOHKLAKKQKPEVEGYAKLEKINAQOLKIOELOEKLEKA----- 648
DB 601 RKATECOHKLAKKQKPEVEGYAKLEKINAQOLKIOELOEKLEKA----- 648
QY 649 ---AKERAERELEKLONRDSSSEGIKKLVAEERRHSLNKVRLLETMERRENRLKOD 704
DB 649 ---AKERAERELEKLONRDSSSEGIKKLVAEERRHSLNKVRLLETMERRENRLKOD 704
QY 705 IOTKSOQIQOMADKILLEBKGRKREAOVSAQHLVHLKQKQYEEKIKYLDNQIKKDLAD 764
DB 705 IOTKSOQIQOMADKILLEBKGRKREAOVSAQHLVHLKQKQYEEKIKYLDNQIKKDLAD 764
QY 720 IOTKSOQIQOMADKILLEBKGRKREAOVSAQHLVHLKQKQYEEKIKYLDNQIKKDLAD 779
DB 720 IOTKSOQIQOMADKILLEBKGRKREAOVSAQHLVHLKQKQYEEKIKYLDNQIKKDLAD 779
QY 765 KETLENMMQORHEEAEHKGKILSEQKAMINAMDSKIRSEQRIVELSEANKLAANSFLT 824
DB 765 KETLENMMQORHEEAEHKGKILSEQKAMINAMDSKIRSEQRIVELSEANKLAANSFLT 824
QY 840 QRMKAQOEEMISELQOKFYLETQAGKEAQNRKLEBOLEKISHODHSPKXNLLLETETL 899
DB 840 QRMKAQOEEMISELQOKFYLETQAGKEAQNRKLEBOLEKISHODHSPKXNLLLETETL 899
QY 885 REVLSLEHBOQKLEKROLTELQLOSERESQUTALQAAALLESQLOKTELESTTEA 944
DB 885 REVLSLEHBOQKLEKROLTELQLOSERESQUTALQAAALLESQLOKTELESTTEA 944
QY 900 REVLSLEHBOQKLEKROLTELQLOSERESQUTALQAAALLESQLOKTELESTTEA 959
DB 900 REVLSLEHBOQKLEKROLTELQLOSERESQUTALQAAALLESQLOKTELESTTEA 959
QY 945 EEEIOALTARDEIORKFDALNSCTVITDLEEQNLQTEBDNAEANNONFYLSKQJDEAS 1004
DB 945 EEEIOALTARDEIORKFDALNSCTVITDLEEQNLQTEBDNAEANNONFYLSKQJDEAS 1004
QY 960 EEEIOALTARDEIORKFDALNSCTVITDLEEQNLQTEBDNAEANNONFYLSKQJDEAS 1019
DB 960 EEEIOALTARDEIORKFDALNSCTVITDLEEQNLQTEBDNAEANNONFYLSKQJDEAS 1019

QY 1005 GANDEIYOLASEVDHLRREITEREMOLTSQKOTMEALKTTCMLERQVMDLEALNDLLE 1064
DB 1020 GANDEIYOLASEVDHLRREITEREMOLTSQKOTMEALKTTCMLERQVMDLEALNDLLE 1079
QY 1065 KERQWEMASVLDSEKSOFECEVRRELQRMIDTEKOSRARADQRTESROVVELAVENHA 1124
DB 1080 KERQWEMASVLDSEKSOFECEVRRELQRMIDTEKOSRARADQRTESROVVELAVENHA 1139
QY 1125 EIALOQALKEQYLKAEBSLSDKINDLEKXAMLENNARSLOQLETERELKORLEBOAK 1184
DB 1140 EIALOQALKEQYLKAEBSLSDKINDLEKXAMLENNARSLOQLETERELKORLEBOAK 1199
QY 1185 LOOQMDLOKXHTPLRLOGLQALDRADLKTESDIEYOLENIQVYSHKXVMEGTIQO 1244
DB 1200 LOOQMDLOKXHTPLRLOGLQALDRADLKTESDIEYOLENIQVYSHKXVMEGTIQO 1259
QY 1245 QTKLIDPLQAKMDQPAKKKGLFSRRKEDPALPTQVPLQYNEIKLLEKARCALEESA 1304
DB 1260 QTKLIDPLQAKMDQPAKKKGLFSRRKEDPALPTQVPLQYNEIKLLEKARCALEESA 1304
QY 1305 LOKTRIELASAREBAHRKATDHPSTPATARQOIAMSAIVRSPEHOPSAMSLAPSS 1364
DB 1305 LOKTRIELASAREBAHRKATDHPSTPATARQOIAMSAIVRSPEHOPSAMSLAPSS 1364
QY 1365 RRKESSTPEEFBRLLKERMHNNIPHRFNGLMMARATKCAVCDTVHFGROASKLECOYM 1424
DB 1365 RRKESSTPEEFBRLLKERMHNNIPHRFNGLMMARATKCAVCDTVHFGROASKLECOYM 1424
QY 1425 CHPKCSTCLPATCGLPABEYATHTFEAFCHDKONSPELOTKESPSSILHEGMMKVPRNNR 1484
DB 1425 CHPKCSTCLPATCGLPABEYATHTFEAFCHDKONSPELOTKESPSSILHEGMMKVPRNNR 1484
QY 1485 GOQGMDRKXIVLEGSVULIYDNEARAGORPIEBEPILCLPDGVSIGHGAVGASELANAK 1544
DB 1485 GOQGMDRKXIVLEGSVULIYDNEARAGORPIEBEPILCLPDGVSIGHGAVGASELANAK 1544
QY 1545 A-----EKAEDAKL 1554
DB 1545 ADVPIYLMKESHPTTCMPGRTLYLLAPSPDKQWVTALESVAGAGRSRKALADAKL 1604
QY 1555 LGNBLILKIEGDRLLDMNCTLPSSDOVYVTEEGLYALNVLKNSLTHVPGIAGVQIYI 1614
DB 1605 LGNBLILKIEGDRLLDMNCTLPSSDOVYVTEEGLYALNVLKNSLTHVPGIAGVQIYI 1664
QY 1615 KOLEKLIMAGEERALCTVDYKVKOSLAQSHLPAPDISPPIFEAVVGCILFGAGKLEN 1674
DB 1665 KOLEKLIMAGEERALCTVDYKVKOSLAQSHLPAPDISPPIFEAVVGCILFGAGKLEN 1724
QY 1675 GLCICAMPSSKVILRYNENLSKCYCIRKEIETSEPCSIHFTNYSILIGTNKFYIDMKO 1734
DB 1725 GLCICAMPSSKVILRYNENLSKCYCIRKEIETSEPCSIHFTNYSILIGTNKFYIDMKO 1784
QY 1735 YLLEFELDKNHSILAPVPAASNSFPVSIQVNSAGOREYLLCTHEFGVCFVDSYGRS 1794
DB 1785 YLLEFELDKNHSILAPVPAASNSFPVSIQVNSAGOREYLLCTHEFGVCFVDSYGRS 1844
QY 1795 RTDILKMSRLPLAFAYREPYLFVTHFNSLEVELEIQAARSAGTPARAYLIDINPRYLGPAT 1854
DB 1845 RTDILKMSRLPLAFAYREPYLFVTHFNSLEVELEIQAARSAGTPARAYLIDINPRYLGPAT 1904
QY 1855 SSGAIYLLASSTQDKIRVICCKGNLVKESGTEHHRPSTSRSSPNKRGPPYNEHTTKVA 1914
DB 1905 SSGAIYLLASSTQDKIRVICCKGNLVKESGTEHHRPSTSRSSPNKRGPPYNEHTTKVA 1964
QY 1915 SSPAPBEGSHPRESTPHRRREGTELRDKSPERPLERKXSGRMISTREESPGRLF 1974
DB 1965 SSPAPBEGSHPRESTPHRRREGTELRDKSPERPLERKXSGRMISTREESPGRLF 2024
QY 1975 BSSSRGRLPAGAVRTPLSQVKKGRGOSASQV 2005
DB 2025 BSSSRGRLPAGAVRTPLSQVKKGRGOSASQV 2055

RESULT 8
US-10-262-511-14
; Sequence 14, Application us/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patuturajan, Weera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malpankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zernusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: Cursaseqdist version 0.1
; SEQ ID NO 14
; LENGTH: 2066
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-14

Query Match 95.4%; Score 10007; DB 15; Length 2066;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1979; Conservative 3; Mismatches 7; Indels 82; Gaps 4;
QY 1 MLKFYGAARNPLDAGAAEPASRASRLNLFQGGKPPFMTQQQWSPLSRGILDALFVLFE 60

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Qy	61	ECGQPLMKIKHNSNVKRSYDITIAELQELQSPAKPEVNSVJGCGHFAVQVVRKATG	120
Db	61	ECGQPLMKIKHNSNVKRSYDITIAELQELQSPAKPEVNSVJGCGHFAVQVVRKATG	120
Qy	121	DIYAMKVMKKALLAOEVSFFEEERNIISRSTSPMIPOLQVAFODKMHLYLMEETQPG	180
Db	121	DIYAMKVMKKALLAOEVSFFEEERNIISRSTSPMIPOLQVAFODKMHLYLMEETQPG	180
Qy	181	DLISLNRREDQDENLQFYLAELILAVNSVHLMGVHRDIXPENILVDRTHIKLVDF	240
Db	181	DLISLNRREDQDENLQFYLAELILAVNSVHLMGVHRDIXPENILVDRTHIKLVDF	240
Qy	241	GSAAKNSNKNVAKPIGTPDYMAPEVLTVMNGDGKITYGLDCCDMSVGVIAEM1YGR	300
Db	241	GSAAKNSNKNVAKPIGTPDYMAPEVLTVMNGDGKITYGLDCCDMSVGVIAEM1YGR	300
Qy	301	SPFAEGTSARTFNINNFORFLKFPDOPKVSDFLDLQSLGQKERLKFEGLCCHPFF	360
Db	301	SPFAEGTSARTFNINNFORFLKFPDOPKVSDFLDLQSLGQKERLKFEGLCCHPFF	360
Qy	361	SKIDMNNIRNSPPFVPTLKSDDTSNFBEPKNSWSSPCQJSPSGFSGEBELPFVGS	420
Db	361	SKIDMNNIRNSPPFVPTLKSDDTSNFBEPKNSWSSPCQJSPSGFSGEBELPFVGS	420
Qy	421	YSKALGILGRSESVGLDSPAATSSMEKKL1KSKBLDSDQKCHMEQEMTRLHRVS	480
Db	421	YSKALGILGRSESVGLDSPAATSSMEKKL1KSKBLDSDQKCHMEQEMTRLHRVS	480
Qy	481	EYBAVLISOKEVELKASSETORSLLEODLATYITECSSIKSLBOARHEVSQEDKALQJH	540
Db	481	EYBAVLISOKEVELKASSETORSLLEODLATYITECSSIKSLBOARHEVSQEDKALQJH	540
Qy	541	DIREOSRKLQEIKEOBYOQAVEEMRLMNOLEEDLVSARRRSDLYSESLAESRLAEFR	600
Db	541	DIREOSRKLQEIKEOBYOQAVEEMRLMNOLEEDLVSARRRSDLYSESLAESRLAEFR	600
Qy	601	KRATBEOHKLKAKDQKPEVGEYAKLEKINAEOQLKIOELOKLEKA-----	648
Db	601	KRATBEOHKLKAKDQKPEVGEYAKLEKINAEOQLKIOELOKLEKA-----	648
Qy	649	-----AEBARLELEKIONREDSSEGI RKTUVEABERRHSENVKRLTETMERENLKD	704
Db	649	-----AEBARLELEKIONREDSSEGI RKTUVEABERRHSENVKRLTETMERENLKD	704
Qy	705	IOTKSQIOQMADKILELEBKREAOVSAQHLVHLKOKOHEEKIKVLDNOIKKOLAD	764
Db	705	IOTKSQIOQMADKILELEBKREAOVSAQHLVHLKOKOHEEKIKVLDNOIKKOLAD	764
Qy	765	KETLENMQRHEEAEHKGKILSEOKAMINAMDSKISLEQRIVELSEANKLAANSFLT	824
Db	765	KETLENMQRHEEAEHKGKILSEOKAMINAMDSKISLEQRIVELSEANKLAANSFLT	824
Qy	825	QANMKAQOEMISLROOKFLETQAGKLEAONKLEBOLKISHOHSDBKRLLEETLU	884
Db	825	QANMKAQOEMISLROOKFLETQAGKLEAONKLEBOLKISHOHSDBKRLLEETLU	884
Qy	885	REVSLEHEBOKLEKXOLTELQSLQERESQLTALAAARALAESOLROAKTELEETAAE	944
Db	885	REVSLEHEBOKLEKXOLTELQSLQERESQLTALAAARALAESOLROAKTELEETAAE	944
Qy	945	EEBIOALTARDEIQRKFDALRNSCTVITDLBEOLNQLTEDNALNNONFYLKQJDEAS	1004
Db	945	EEBIOALTARDEIQRKFDALRNSCTVITDLBEOLNQLTEDNALNNONFYLKQJDEAS	1004
Qy	1005	GANDEIVOLRSEVDHRRREITEREMQTSQKQMEALKTCTMLBEQVMDLELNBELLE	1064
Db	1005	GANDEIVOLRSEVDHRRREITEREMQTSQKQMEALKTCTMLBEQVMDLELNBELLE	1064
Qy	1065	KEROWEAMSVLGDSEKQFECRVRLEORMDTEKOSRARADORTSSROVELAVKXENKA	1124
Db	1065	KEROWEAMSVLGDSEKQFECRVRLEORMDTEKOSRARADORTSSROVELAVKXENKA	1124

Db	1080	KEROWEAMSVLGDSEKQFECRVRLEORMDTEKOSRARADORTSSROVELAVKXENKA	1139
Qy	1125	ETIALQOALKEQKLAESISDLKNDLEKKAHLENNARSLOOKLETERELKORLEBOAK	1184
Db	1140	ETIALQOALKEQKLAESISDLKNDLEKKAHLENNARSLOOKLETERELKORLEBOAK	1199
Qy	1185	LOOQMDLOKNNHIFRLTOGLQELADRLKTERSDLEYOLENIQVLYSHEKVMETTSQ	1244
Db	1200	LOOQMDLOKNNHIFRLTOGLQELADRLKTERSDLEYOLENIQVLYSHEKVMETTSQ	1259
Qy	1245	QTKLIDFLQAKNDQPAKXXXXXFSRRKEDPALPTQVLOYNELKJALEKAKCALEBA	1304
Db	1260	QTKLIDFLQAKNDQPAKXXXXXFSRRKEDPALPTQVLOYNELKJALEKAKCALEBA	1304
Qy	1305	LOKTRIELSARBEAARAKATDHPHSPATARQOIMASAIYRSPHOSASMLAPSS	1364
Db	1305	LOKTRIELSARBEAARAKATDHPHSPATARQOIMASAIYRSPHOSASMLAPSS	1364
Qy	1365	RRKESSTPEFRRILKERMHNNI PHRFNVGLNMRATKCAVCLDTYHFGQASKECQVM	1424
Db	1365	RRKESSTPEFRRILKERMHNNI PHRFNVGLNMRATKCAVCLDTYHFGQASKECQVM	1424
Qy	1425	CHPKSCTCLPATCGLPABEYATHTFAFCRDKNNSPGLQTKBSSSLHLEGMMKVPRNNR	1484
Db	1425	CHPKSCTCLPATCGLPABEYATHTFAFCRDKNNSPGLQTKBSSSLHLEGMMKVPRNNR	1484
Qy	1485	GOQMDRKTYILEGKSVL1YDNEABAGORPVEEBELCLPDGDVSIHGAVGASLANTAK	1544
Db	1485	GOQMDRKTYILEGKSVL1YDNEABAGORPVEEBELCLPDGDVSIHGAVGASLANTAK	1544
Qy	1545	A-----EKAEDATL	1554
Db	1545	A-----EKAEDATL	1554
Qy	1555	LGNSLLKLEGDDRLDMNCTLPSPDOVVLVGTBEGYALANVLKNSLTHVIGAVPQIY11	1614
Db	1605	LGNSLLKLEGDDRLDMNCTLPSPDOVVLVGTBEGYALANVLKNSLTHVIGAVPQIY11	1664
Qy	1615	KOLEKLM1AGEBRALCLVDYKVKQSLAOSHLPAQOPDISPNIPEAVKCHLFGAKTEN	1674
Db	1665	KOLEKLM1AGEBRALCLVDYKVKQSLAOSHLPAQOPDISPNIPEAVKCHLFGAKTEN	1724
Qy	1675	GLCTAAMPSSKVILRYNENLSKYCIKREIETSEBSCSIHFNYSILGTNKFEYIDMKO	1734
Db	1725	GLCTAAMPSSKVILRYNENLSKYCIKREIETSEBSCSIHFNYSILGTNKFEYIDMKO	1784
Qy	1735	YTLBEFLDKNDHSLPAVFAASNSFPVSIQVNSAGOREBYLCTFHERGVFVDSYGRS	1794
Db	1785	YTLBEFLDKNDHSLPAVFAASNSFPVSIQVNSAGOREBYLCTFHERGVFVDSYGRS	1844
Qy	1795	RTDDLKWSRLPLAFAYREBYLFTYHNSILEVIEIOARSSAGTPADAYLDIPNRYLGPAI	1854
Db	1845	RTDDLKWSRLPLAFAYREBYLFTYHNSILEVIEIOARSSAGTPADAYLDIPNRYLGPAI	1904
Qy	1855	SSGATYLLASSYODKRLVYCKKCNLVKESGTEHHRPSTSRSSPNRGPPTVNEHTTKRA	1914
Db	1905	SSGATYLLASSYODKRLVYCKKCNLVKESGTEHHRPSTSRSSPNRGPPTVNEHTTKRA	1964
Qy	1915	SSPAPPEGSHPRESTPHRYREGRTELRLRDSPPRPLEREKSPGRMLSTRERSPGRLF	1974
Db	1965	SSPAPPEGSHPRESTPHRYREGRTELRLRDSPPRPLEREKSPGRMLSTRERSPGRLF	2024
Qy	1975	EDSSRGRLPAGAVRTPLSQVNGKQASQV	2005
Db	2025	EDSSRGRLPAGAVRTPLSQVNGKQASQV	2055

RESULT 2

US-09-964-956-11
; Sequence 11, Application US/09964956
; Publication No. US20040043926A1
; GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L

```
/ APPLICANT: MacDougall, John R
/ APPLICANT: Smithson, Glenda
/ APPLICANT: Millet, Isabelle
/ APPLICANT: Stone, David
/ APPLICANT: Gunther, Erik
/ APPLICANT: Ellerman, Karen
/ APPLICANT: Grose, William M
/ APPLICANT: Alsobrook II, John P
/ APPLICANT: Lepley, Denise M
/ APPLICANT: Burgess, Catherine E
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Kexuda, Ramesh
/ APPLICANT: Spytek, Kimberly A
/ APPLICANT: Leach, Martin D
/ APPLICANT: Shinkets, Richard A
/ TITLE OF INVENTION: No. US20040043926A1el Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-124
/ CURRENT APPLICATION NUMBER: US/09/964,956
/ CURRENT FILING DATE: 2001-09-26
/ PRIOR APPLICATION NUMBER: 60/235,631
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: 60/235,633
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: 60/235,808
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: 60/236,064
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: 60/236,065
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: 60/236,066
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: 60/236,135
/ PRIOR FILING DATE: 2000-09-28
/ PRIOR APPLICATION NUMBER: 60/237,434
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/238,321
/ PRIOR FILING DATE: 2000-10-05
/ PRIOR APPLICATION NUMBER: 60/238,399
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: 60/238,396
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: 60/276,667
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/294,823
/ PRIOR FILING DATE: 2001-05-31
/ PRIOR APPLICATION NUMBER: 60/304,868
/ PRIOR FILING DATE: 2001-07-12
/ NUMBER OF SEQ ID NOS: 127
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 11
/ LENGTH: 2053
/ TYPE: prt
/ ORGANISM: Homo sapiens
/ US-09-964-956-11

Query Match      95.4%; Score 10005; DB 11; Length 2053;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1978; Conservative 3; Mismatches 5; Indels 82; Gaps 4;
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181 DLLSLNRYEDQDENLIGFYLAELILAVSHVLMGYVRDIPENILVDRGTGKLYDF 240
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241 GSAATNSNKNMNAKLPIGTPDYMAPEVLTWNNGCKTYGDCDMSVGVAYEMYGR 300
Db
241 GSAATNSNKN -VNAKLPIGTPDYMAPEVLTWNNGCKTYGDCDMSVGVAYEMYGR 299
QY
301 SPFAEGTSARTPNNIMNFORFLKPPDPKVSDFDLIQSLLCQGERLKFCGHPFF 360
Db
300 SPFAEGTSARTPNNIMNFORFLKPPDPKVSDFDLIQSLLCQGERLKFCGHPFF 359
QY
361 SKIDWNINRNSPPFPVPTLKSDDTSNFDEPKNSWSSSPCLSPSGSGELPFVGRS 420
Db
360 SKIDWNINRNSPPFPVPTLKSDDTSNFDEPKNSWSSSPCLSPSGSGELPFVGRS 419
QY
421 YKALGILIGRSSVYSGIDSPAKTSMERKLLIKKELQDSQDKHKEQENTRLHRRVS 480
Db
420 YKALGILIGRSSVYSGIDSPAKTSMERKLLIKKELQDSQDKHKEQENTRLHRRVS 479
QY
481 EYEAVALSQKEVELKASRTORSILJEODLATYITECSLSKRSLEQAMEVSOEDKALQLLH 540
Db
480 EYEAVALSQKEVELKASRTORSILJEODLATYITECSLSKRSLEQAMEVSOEDKALQLLH 539
QY
541 DIREQSRKLQEIKEQEOYAQVEEMLMNQLBEDLVASARRSDLYESILRESRLAEEFK 600
Db
540 DIREQSRKLQEIKEQEOYAQVEEMLMNQLBEDLVASARRSDLYESILRESRLAEEFK 599
QY
601 KRATCOHKLKAKQOGKPEVGEFVAKLEKINAEOQLKQEOEKLEKVKASTEATELLQ 659
Db
600 KRATCOHKLKAKQOGKPEVGEFVAKLEKINAEOQLKQEOEKLEKVKASTEATELLQ 649
QY
649 ----AKERAERLEKLONRDEDSSEGIKKLVEAERRSLKVRLETMERENRLKDD 704
Db
660 NIRAKEAERLEKLONRDEDSSEGIKKLVEAERRSLKVRLETMERENRLKDD 719
QY
705 IQTKSQOIQQVADKILLEBKREAVSAQHLVHLKQEOHYEBEKIIVLDNQIKDLAD 764
Db
720 IQTKSQOIQQVADKILLEBKREAVSAQHLVHLKQEOHYEBEKIIVLDNQIKDLAD 779
QY
765 KETLENMQRHHEEHKGIILSEQKAMINMDSKIRLEQRIYVLSANKLAANSILFT 824
Db
780 KETLENMQRHHEEHKGIILSEQKAMINMDSKIRLEQRIYVLSANKLAANSILFT 839
QY
825 QRNMKAQEBMISLQOQFYLETQAGKLEAQRKLEBELEKISHQDHDKRNLLLEFRL 884
Db
840 QRNMKAQEBMISLQOQFYLETQAGKLEAQRKLEBELEKISHQDHDKRNLLLEFRL 899
QY
885 REVSLHEHQKLELRQULTBELQSLQERESQULTALQAAPALLESQLRQAKTELEETTAA 944
Db
900 REVSLHEHQKLELRQULTBELQSLQERESQULTALQAAPALLESQLRQAKTELEETTAA 959
QY
945 EEEIQALTNRHDEIQKFDALRNSCTVITDLEEQUNOLTENDNAELNNOFFYLSKOLDERS 1004
Db
960 EEEIQALTNRHDEIQKFDALRNSCTVITDLEEQUNOLTENDNAELNNOFFYLSKOLDERS 1019
QY
1005 GANDEIYOLRSVVDHLRREITEREMQULTSOKQIYMALKTTCMTLEEOYVWDLLEALDELLE 1064
Db
1020 GANDEIYOLRSVVDHLRREITEREMQULTSOKQIYMALKTTCMTLEEOYVWDLLEALDELLE 1079
QY
1065 KERQWEANRSVLDGDEKSQFECVRLEQLMDTEKQSRARADQRTITESQVAVELAVKEHA 1124
Db
1080 KERQWEANRSVLDGDEKSQFECVRLEQLMDTEKQSRARADQRTITESQVAVELAVKEHA 1139
QY
1125 ETLALQALKEQKLAESLSDPLNLEKGMALFNNAASLQOKLETREBELKORLLEBOAK 1184
Db
1140 ETLALQALKEQKLAESLSDPLNLEKGMALFNNAASLQOKLETREBELKORLLEBOAK 1199
QY
1185 LQQQMDLQKNHIFRLTOGLOEALDRADLLKTERSDLEYOLENIQVLYSHKEKYMGEGTISQ 1244
Db
1200 LQQQMDLQKNHIFRLTOGLOEALDRADLLKTERSDLEYOLENIQVLYSHKEKYMGEGTISQ 1259
QY
1245 QTKLIDFLQAKMDQPAKKKKGLFSRRKEDPALPTQVPLQVNELKLALKEKARCALBEA 1304
Db
1260 QTKLIDFLQAKMDQPAKKKK-----VPLQVNELKLALKEKARCALBEA 1304
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Db      300 SPFAEGSARTFNMINMFQRFLLKFPDDPKVSSDFLDLIGSLGCGKRLKFBGLCHCHPFF 359
Qy      361 SKIDMNNIRSPFPVPTLLKSDDDTGNFDEPENSWSSPCQLSPSGSGEELPVYVGS 420
Db      360 SKIDMNNIRNAPFPVPTLLKSDDDTGNFDEPENSWSSPCQLSPSGSGEELPVYVGS 419
Qy      421 YSKALGILGRSESVGLDSPAFTKSSMEKLLIKSKELDSDPKCHMEQEMRLRRYS 480
Db      420 YSKALGILGRSESVGLDSPAFTKSSMEKLLIKSKELDSDPKCHMEQEMRLRRYS 479
Qy      481 EYVAIVISQKEVELKASFTORSLLLEODLATTTECSSLSKSLSEQARMEVSGEDDKALQLH 540
Db      480 EYVAIVISQKEVELKASFTORSLLLEODLATTTECSSLSKSLSEQARMEVSGEDDKALQLH 539
Qy      541 DIIEOGRKLOEIKEOEYQAVEEMRLMMNOLLEEDLYSARRSDLYSESLRESLABERK 600
Db      540 DIIEOGRKLOEIKEOEYQAVEEMRLMMNOLLEEDLYSARRSDLYSESLRESLABERK 599
Qy      601 RKATECOHLLKAKDOGKPEVGEYAKLEKINAEQQLKIOELQKLEKA----- 648
Db      600 RKATECOHLLKAKDOGKPEVGEYAKLEKINAEQQLKIOELQKLEKAVKASTEATELLQ 659
Qy      649 ----AERABRELKTIQNRDSESGIRKKLVAEERHSLNKKLEETMERRENKLKD 704
Db      660 NIRAOKARERLEKLONERDESSEGIKKLVAEERHSLNKKLEETMERRENKLKD 719
Qy      705 IOTKSQOIQOMADKILEBEKREAVSNOHLEVHIKOEQYHEEKITLNDQIKDLD 764
Db      720 IOTKSQOIQOMADKILEBEKREAVSNOHLEVHIKOEQYHEEKITLNDQIKDLD 779
Qy      765 KETLENMORHEBEAHEKGIKILSEQKAMINAMDSKIRSEORIVELSEANKLAANSFLT 824
Db      780 KETLENMORHEBEAHEKGIKILSEQKAMINAMDSKIRSEORIVELSEANKLAANSFLT 839
Qy      825 QNRNMQAEEMISLROQKYTLTQAGKLEAONRKLEBOLEKISHODHSXNRLLEETL 884
Db      840 QNRNMQAEEMISLROQKYTLTQAGKLEAONRKLEBOLEKISHODHSXNRLLEETL 899
Qy      885 REVSLHEBOKLEKROKTELQLOESRESQLTALQARALSESQROKTELEETL 944
Db      900 REVSLHEBOKLEKROKTELQLOESRESQLTALQARALSESQROKTELEETL 959
Qy      945 EEEIQAALYARDEIQKRFALNSCTVTITDLEBOLNQLTEDNAELNNQNFYLSKOLDEAS 1004
Db      960 EEEIQAALYARDEIQKRFALNSCTVTITDLEBOLNQLTEDNAELNNQNFYLSKOLDEAS 1019
Qy      1005 GANDEIVQARSVDHRRREITEREMQUTSQKOTMEALKTTCTMLEBOVMDLEALDELIE 1064
Db      1020 GANDEIVQARSVDHRRREITEREMQUTSQKOTMEALKTTCTMLEBOVMDLEALDELIE 1079
Qy      1065 KERQWEAMRSVLGDEKSOFECEVRELQRMIDTEKOSBARADORITESROVVELAYKEHA 1124
Db      1080 KERQWEAMRSVLGDEKSOFECEVRELQRMIDTEKOSBARADORITESROVVELAYKEHA 1139
Qy      1125 ELIALQALKEQKLAESISDKLNDLEKKHAMELNARSLOOKLETERELKORLLEBOAK 1184
Db      1140 ELIALQALKEQKLAESISDKLNDLEKKHAMELNARSLOOKLETERELKORLLEBOAK 1199
Qy      1185 LQQQMDLQKNHI FRLTQGLQELADRADLKTFRSLEYOLENIQVLYSHKRYMGGTISQ 1244
Db      1200 LQQQMDLQKNHI FRLTQGLQELADRADLKTFRSLEYOLENIQVLYSHKRYMGGTISQ 1259
Qy      1245 QTKLIDFLQAKMDQPAKKKGLFSRRKEDPALPTQVPLQVNLKLALEKXARCALEBA 1304
Db      1260 QTKLIDFLQAKMDQPAKKKGLFSRRKEDPALPTQVPLQVNLKLALEKXARCALEBA 1304
Qy      1305 LOKTRIEBSAREEBAHRAVTDHPSPATARQOJAMSAYRSBEHOPAMSLLAPPS 1364
Db      1305 LOKTRIEBSAREEBAHRAVTDHPSPATARQOJAMSAYRSBEHOPAMSLLAPPS 1364
Qy      1365 RKKESTPEBFSRRLKERHNNHIIHRFVNGLMARATKCAVCLDVTYHFGROASKLECOVM 1424

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Db      1365 RKKESTPEBFSRRLKERHNNHIIHRFVNGLMARATKCAVCLDVTYHFGROASKLECOVM 1424
Qy      1425 CHPKCSTCLPATCGIPAEYATHFTPAFCRDKNNSGLOTEPSSLIHEGMKVPRNNKR 1484
Db      1425 CHPKCSTCLPATCGIPAEYATHFTPAFCRDKNNSGLOTEPSSLIHEGMKVPRNNKR 1484
Qy      1485 GQGWDRKTYLVEGSKVLIYDNEARAGORPVEEBELCLPODDVSIHGAVGASELANYAK 1544
Db      1485 GQGWDRKTYLVEGSKVLIYDNEARAGORPVEEBELCLPODDVSIHGAVGASELANYAK 1544
Qy      1545 A-----EKAERADKL 1554
Db      1545 ADVPYILKMHESHPTTCGRTLYLLAPSFPDQKWTALBSVAGRVSRKADAKL 1604
Qy      1555 LGNSLLKLEGGDRLLDMNCTLPSPDOVYVGTREBGILYALNVKNSLTHYPGIGAVQIYII 1614
Db      1605 LGNSLLKLEGGDRLLDMNCTLPSPDOVYVGTREBGILYALNVKNSLTHYPGIGAVQIYII 1664
Qy      1615 KOLEKLMIMAGEBALCLVDYKVKVQSLAQSHLPAPQDISPNIPEAVKGCILFGAGKLEN 1674
Db      1665 KOLEKLMIMAGEBALCLVDYKVKVQSLAQSHLPAPQDISPNIPEAVKGCILFGAGKLEN 1724
Qy      1675 GLCICAMPKSVVILRYNENISKYCIRKEIETSEPCSCIHFTNYSILIGTKKFEYIDMKO 1734
Db      1725 GLCICAMPKSVVILRYNENISKYCIRKEIETSEPCSCIHFTNYSILIGTKKFEYIDMKO 1784
Qy      1735 YLLEEFLLKNDHSLAPYAPFAASNSFPVSIYQVNSAGREBYLLCFHEFGYFVDSYGRS 1794
Db      1785 YLLEEFLLKNDHSLAPYAPFAASNSFPVSIYQVNSAGREBYLLCFHEFGYFVDSYGRS 1844
Qy      1795 RTDCLKMSRLPLAFAYREPLYFVTHFNLSLEYIEIQARSAGTPARAYVDINPRTYIGPAI 1854
Db      1845 RTDCLKMSRLPLAFAYREPLYFVTHFNLSLEYIEIQARSAGTPARAYVDINPRTYIGPAI 1904
Qy      1855 SSGAIYLAASYQDKLRVICCKGNLVKESGTEHHRGPSTSRSSPNKRGPTYNENHITKVA 1914
Db      1905 SSGAIYLAASYQDKLRVICCKGNLVKESGTEHHRGPSTSRSSPNKRGPTYNENHITKVA 1964
Qy      1915 SSPAPBGPSPHREESTPHRRRREGRTELRRPKSGRPLERKSGRMISTREBSFGSLF 1974
Db      1965 SSPAPBGPSPHREESTPHRRRREGRTELRRPKSGRPLERKSGRMISTREBSFGSLF 2024
Qy      1975 EDSRGRPLPAGAVTPTLSQVANKRGQSA 2002
Db      2025 EDSRGRPLPAGAVTPTLSQVANKRGQSA 2052

RESULT 11
US-10-017-216-4
; Sequence 4, Application US/10017216
; Publication No. US20020160483A1
; GENERAL INFORMATION:
; APPLICANT: KAPELIER-LIBERMANN, Rosana
; TITLE OF INVENTION: 13245, A No. US20020160483A1el Human Myotonic Dystrophy Type Prot
; FILE REFERENCE: 10147-5701
; CURRENT APPLICATION NUMBER: US/10/017, 216
; PRIOR APPLICATION NUMBER: US 60/242,429
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2055
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-017-216-4

Query Match      92.0%; Score 9656; DB 13; Length 2055;
Best Local Similarity 91.9%; Pred. No. 0;
Matches 1903; Conservative 41; Mismatches 42; Indels 84; Gaps 5;

Qy      1 MLKFKYGARNPLDAGAAEPASRLNLPFGKPPMTQOQMSPLSREGILDALFVLFE 60

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Db 1 MLKFKGVNRPBASASEPIASASRLNLFQCKPPLMTQOQOQSALSRGMDALPALRE 60
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 Db 61 ECGOPALMKIKIVSNVNRKYSOTLTAELOEPASAKPEVRSVGVCGHFAEVOVREKATG 120
 Qy 121 D1YAMVMMKKALLAOEOWSPFEERNTIISRTSPMIPOLOVAFOOKNLYLMEEQOPG 180
 Db 121 D1YAMVMMKKALLAOEOWSPFEERNTIISRTSPMIPOLOVAFOOKNLYLMEEQOPG 180
 Qy 181 DL1SLNRYEDOLDEMLIOFYLAELILAAVSHVMGVHRDIPENILVDRTHIKLVPE 240
 Db 181 DL1SLNRYEDOLDEMLIOFYLAELILAAVSHVMGVHRDIPENILVDRTHIKLVPE 240
 Qy 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMNGDGKTYGLDCDMWSVGVIAVEM1YGR 300
 Db 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMNGDGKTYGLDCDMWSVGVIAVEM1YGR 300
 Qy 301 SEPABEATSARTPNINNFQRFLEKFPDDPKVSSDFLLIQSLCQGERLKFEGLCCHPFF 360
 Db 301 SEPABEATSARTPNINNFQRFLEKFPDDPKVSSDFLLIQSLCQGERLKFEGLCCHPFF 360
 Qy 361 SKIDMNNIRNSPPFPVPTLKSDDOTSNFDEPEKNSWSSPCQLSPSGFSGEELPVPVGS 420
 Db 361 SKIDMNNIRNSPPFPVPTLKSDDOTSNFDEPEKNSWSSPCQLSPSGFSGEELPVPVGS 420
 Qy 421 YSKALGILGRSESVSGSDSPAKTSSMEKKL1KSKELQSDQDKHMEQEMTRLRHVS 480
 Db 421 YSKALGILGRSESVSGSDSPAKTSSMEKKL1KSKELQSDQDKHMEQEMTRLRHVS 480
 Qy 481 EYEAVALSQEVELKASETORSLLEODLATYITECSSLSKSLBEAPRMEVQEOEDKALQLH 540
 Db 481 EYEAVALSQEVELKASETORSLLEODLATYITECSSLSKSLBEAPRMEVQEOEDKALQLH 540
 Qy 541 D1REGOSRKOETKEOQYQAOVEEMRLMMNOLEEDLVASARRSDLYSESLRESLAAEPFK 600
 Db 541 D1REGOSRKOETKEOQYQAOVEEMRLMMNOLEEDLVASARRSDLYSESLRESLAAEPFK 600
 Qy 601 RKATECOHKLAKADQKPEVGEYATLEKINAEQOLKIOLOEKLEKA----- 648
 Db 601 RKATECOHKLAKADQKPEVGEYATLEKINAEQOLKIOLOEKLEKA----- 648
 Qy 649 ----AKERARELEKLONRDSESGIRKCLVEABERRSHLENKVKLETMERRENKLOD 704
 Db 649 ----AKERARELEKLONRDSESGIRKCLVEABERRSHLENKVKLETMERRENKLOD 704
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 Db 705 IOTKSOQIOOMADKILEEKHREAOVSAQHLEVHLKQKQHYEEKIKYLDNQIKKDLAD 764
 Qy 765 KETLEMMORHEEAEHEKGI1SEQKAMINAMDSKIRLEQRIVEKSEANKLAANSFLT 824
 Db 765 KETLEMMORHEEAEHEKGI1SEQKAMINAMDSKIRLEQRIVEKSEANKLAANSFLT 824
 Qy 825 QRNMKAQOEMISELROOKFYLETQAGKLEAONKLEBOLEKISHODSDKNLLLEETRL 884
 Db 825 QRNMKAQOEMISELROOKFYLETQAGKLEAONKLEBOLEKISHODSDKNLLLEETRL 884
 Qy 885 REVSLEHEBOKLEKQOLTELQSLQBRBSQLTALQAAAPAALESQURQAKTELEETTA 944
 Db 885 REVSLEHEBOKLEKQOLTELQSLQBRBSQLTALQAAAPAALESQURQAKTELEETTA 944
 Qy 945 EBEIQAULTAHARDEIQKFDALRNSCTVITDLBEQOLNQLTEDNAELNNONFYLSKQDEAS 1004
 Db 945 EBEIQAULTAHARDEIQKFDALRNSCTVITDLBEQOLNQLTEDNAELNNONFYLSKQDEAS 1004
 Qy 1005 GANDEIYOLRSEVDHLRREITEREMQ1TSQQTMEALKTTCTMLEEQVNDLEALNDELLE 1064
 Db 1005 GANDEIYOLRSEVDHLRREITEREMQ1TSQQTMEALKTTCTMLEEQVNDLEALNDELLE 1064
 Qy 1020 GANDEIYOLRSEVDHLRREITEREMQ1TSQQTMEALKTTCTMLEEQVNDLEALNDELLE 1079
 Db 1020 GANDEIYOLRSEVDHLRREITEREMQ1TSQQTMEALKTTCTMLEEQVNDLEALNDELLE 1079
 Qy 1065 KERQWAMNSVLDGEKSOFCREVRREIQMLDTEKORAPADQOITSSQVVELAVEHKA 1124
 Db 1065 KERQWAMNSVLDGEKSOFCREVRREIQMLDTEKORAPADQOITSSQVVELAVEHKA 1124

Db 1080 KERQWAMNSVLDGEKSOFCREVRREIQMLDTEKORAPADQOITSSQVVELAVEHKA 1139
 Qy 1125 ETLALQALKEOKLAESISDNLNLEKKAHLENNANSLOOKLETERELKORLLEBOAK 1184
 Db 1140 ETLALQALKEOKLAESISDNLNLEKKAHLENNANSLOOKLETERELKORLLEBOAK 1199
 Qy 1185 LQOQMDLOKNHIFRLTQGLQEZALDRADLLKTERSDLEYOLENIQVLYSHKEKMEGTISQ 1244
 Db 1200 LQOQMDLOKNHIFRLTQGLQEZALDRADLLKTERSDLEYOLENIQVLYSHKEKMEGTISQ 1259
 Qy 1245 QTKLIDFLQAKKDOPAKKKKGLFSRRKEDPALPTQVPLQYNELKLALEKAKACALEBA 1304
 Db 1260 QTKLIDFLQAKKDOPAKKKKGLFSRRKEDPALPTQVPLQYNELKLALEKAKACALEBA 1304
 Qy 1305 LQKTRIELRSABEAAHRAKATHTHPSTPATRQO1AMSAIYRSPEHOSAMSILAPSS 1364
 Db 1305 LQKTRIELRSABEAAHRAKATHTHPSTPATRQO1AMSAIYRSPEHOSAMSILAPSS 1364
 Qy 1365 RRKESSTPEEFSRRLKERMHNI1PHRFNVGLMNRATKCAVCLDTVHFGQASKLECOYM 1424
 Db 1365 RRKESSTPEEFSRRLKERMHNI1PHRFNVGLMNRATKCAVCLDTVHFGQASKLECOYM 1424
 Qy 1425 CHPKSCTCLPATCGLPABYATHTTEAFCDKXNSPGLQTKESPSSILHEGMKVPRNNKR 1484
 Db 1425 CHPKSCTCLPATCGLPABYATHTTEAFCDKXNSPGLQTKESPSSILHEGMKVPRNNKR 1484
 Qy 1485 GOQGDRTKTYLEGSVLYLYDNABABAGORPVEEBFLCLPDQDVS1HGVASSELANTAK 1544
 Db 1485 GOQGDRTKTYLEGSVLYLYDNABABAGORPVEEBFLCLPDQDVS1HGVASSELANTAK 1544
 Qy 1545 A-----EKAEADATL 1554
 Db 1545 A-----EKAEADATL 1554
 Qy 1555 LGNSILKLEGGDRDLDMNCTLPESDQVYLVGTEEGYALANLVNLSLTHVPBG1GAVFOIY11 1614
 Db 1605 LGNSILKLEGGDRDLDMNCTLPESDQVYLVGTEEGYALANLVNLSLTHVPBG1GAVFOIY11 1664
 Qy 1615 KOLEKLM1AGEBRALCLVDVKKVQSLAQSHLPAPODIS1PNI1FEAVKCGHL1FAGK1EN 1674
 Db 1665 KOLEKLM1AGEBRALCLVDVKKVQSLAQSHLPAPODIS1PNI1FEAVKCGHL1FAGK1EN 1724
 Qy 1675 GLC1GAMPSKVY11RYNEN1SKYCIKREIETSEPCSH1FTNYSL1LGTNKFYE1DMKO 1734
 Db 1725 GLC1GAMPSKVY11RYNEN1SKYCIKREIETSEPCSH1FTNYSL1LGTNKFYE1DMKO 1784
 Qy 1735 YTLBEFLDKNDS1LAPVPAASSNSFPVSIYVANSAGOREBYILCFHEBGFVDSYGRS 1794
 Db 1785 YTLBEFLDKNDS1LAPVPAASSNSFPVSIYVANSAGOREBYILCFHEBGFVDSYGRS 1844
 Qy 1795 RTDDLKMSRLPLAFVREBYLFTVHNSLEVI1EQARSSAGTPPARAYLD1PNPRYLGPA1 1854
 Db 1845 RTDDLKMSRLPLAFVREBYLFTVHNSLEVI1EQARSSAGTPPARAYLD1PNPRYLGPA1 1904
 Qy 1855 SSGAIY1LASSYODK1RV1CCKNLVKESGTEHHRGPSTRSASPNNKRGPTTYHEHTKRA 1914
 Db 1905 SSGAIY1LASSYODK1RV1CCKNLVKESGTEHHRGPSTRSASPNNKRGPTTYHEHTKRA 1964
 Qy 1915 SSPAPPEGSHPRBSTPHRY--REGRTELARDKSPGRPLEBEKSPGRMLSTRERSPOR 1972
 Db 1965 SSPAPPEGSHPRBSTPHRY--REGRTELARDKSPGRPLEBEKSPGRMLSTRERSPOR 2024
 Qy 1973 LFEDESSRGLPAGAVRTP1LSQVNNKRGQSA 2002
 Db 2025 LFEDESSRGLPAGAVRTP1LSQVNNKRGQSA 2054

RESULT 12
 US-10-028-946-4
 ; Sequence 4, Application US/10028946
 ; Publication No. US20020123622A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yu, Xuanchuan

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/ APPLICANT: Miranda, Maricar
/ APPLICANT: Fridde, Carl Johan
/ TITLE OF INVENTION: No US20020123622A1el Human kinases and Polynucleotides Encoding
/ FILE REFERENCE: LEX-0289-USA
/ CURRENT APPLICATION NUMBER: US/10/028,946
/ PRIOR FILING DATE: 2001-12-20
/ PRIOR APPLICATION NUMBER: US 60/258,335
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 1958
/ TYPE: PRF
/ ORGANISM: homo sapiens
/ US-10-028-946-4

Query Match      90.4%; Score 9487.5; DB 13; Length 1958;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 1877; Conservative 1; Mismatches 1; Indels 81; Gaps 3;

QY      1 MTKFKYGANNPLDAGAAEPPIASASRLNLFQCKPPEPMTQQOMSPLSREGIILDALFVLE 60
DB      1 MTKFKYGANNPLDAGAAEPPIASASRLNLFQCKPPEPMTQQOMSPLSREGIILDALFVLE 60
QY      61 ECSQPALMKIKHVSNFVRKYSDTIAELOEPSAKDFEYRSIVGCGHFAVQVREKATG 120
DB      61 ECSQPALMKIKHVSNFVRKYSDTIAELOEPSAKDFEYRSIVGCGHFAVQVREKATG 120
QY      121 DIYAMKVMKKALLAQEQVSPFEEERNILSRSTSPWIPOLQYAFODKNHLYIMEEYOPG 180
DB      121 DIYAMKVMKKALLAQEQVSPFEEERNILSRSTSPWIPOLQYAFODKNHLYIMEEYOPG 180
QY      181 DILBLINRYEDQDENLQFYLAELILAHVSYHLMGYARDIKPENIILVDRGHITLQNF 240
DB      181 DILBLINRYEDQDENLQFYLAELILAHVSYHLMGYARDIKPENIILVDRGHITLQNF 240
QY      241 GSAAKNNSNMVNAKLPIDTPYMAPEVLTVMNGDGKGTGGLDCMWSVGIAYEMIYGR 300
DB      241 GSAAKNNSNMVNAKLPIDTPYMAPEVLTVMNGDGKGTGGLDCMWSVGIAYEMIYGR 300
QY      301 SPFASTGARTNNINMFORPLKPPDDPVSSDFLDLIQSLICGQKERLKFEGLCCHPFF 360
DB      301 SPFASTGARTNNINMFORPLKPPDDPVSSDFLDLIQSLICGQKERLKFEGLCCHPFF 360
QY      361 SKIDMNNINSPFPVPTLKSDDDTSNPDPEKNSVSSPCQLSPSGSGSELPPVGS 420
DB      361 SKIDMNNINSPFPVPTLKSDDDTSNPDPEKNSVSSPCQLSPSGSGSELPPVGS 420
QY      421 YSKALGILGRSESVSGLDSPAKTSMKKLTKSKELQDSQDKCHMQEOMTRLHRRYS 480
DB      421 YSKALGILGRSESVSGLDSPAKTSMKKLTKSKELQDSQDKCHMQEOMTRLHRRYS 480
QY      481 EYEAIVLSQKEVVLKASETORSLLEODLATYITECSSLKRSLEQAMNEVSQEDDKALQLH 540
DB      481 EYEAIVLSQKEVVLKASETORSLLEODLATYITECSSLKRSLEQAMNEVSQEDDKALQLH 540
QY      541 DIRBOSRKLOEIKOEBOYQAOVEEMRLMNOLEEDIVSARRSDIVSESLRESRLAAEPK 600
DB      541 DIRBOSRKLOEIKOEBOYQAOVEEMRLMNOLEEDIVSARRSDIVSESLRESRLAAEPK 600
QY      601 RKATECOHKLAKQDKGPEVEYAKLEKINAQOOLQLOEOLKEKA----- 648
DB      601 RKATECOHKLAKQDKGPEVEYAKLEKINAQOOLQLOEOLKEKA----- 648
QY      649 ----AKERAERLEKLONEEDSSEGIKKLVEAEBRRHSLNKKVRLFTMERRENRLKMD 704
DB      661 NIROAKERERLEKLONEEDSSEGIKKLVEAEBRRHSLNKKVRLFTMERRENRLKMD 720
QY      705 IOTKSOQIOQMADKLTLEEKHREAOVSAOHLEVHLKOEKOHYEKIKTLDMQIKKDLAD 764
DB      721 IOTKSOQIOQMADKLTLEEKHREAOVSAOHLEVHLKOEKOHYEKIKTLDMQIKKDLAD 780
QY      765 KETLENMQRHEEAHEKGIILSEQKAMINAMDSKIRLEQRIVELSEANKLAANSLSFT 824
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DB      781 KETLENMQRHEEAHEKGIILSEQKAMINAMDSKIRLEQRIVELSEANKLAANSLSFT 840
QY      825 QNMKAQEBMISELFOQKPYLETQAGKLEPAONRKLEOLEKISHODSDKNLLETRL 884
DB      841 QNMKAQEBMISELFOQKPYLETQAGKLEPAONRKLEOLEKISHODSDKNLLETRL 900
QY      885 REVSLHEHQKLEKROLTLEOLSLQERESQLTALQARALLESQROAKTELESTTBA 944
DB      901 REVSLHEHQKLEKROLTLEOLSLQERESQLTALQARALLESQROAKTELESTTBA 960
QY      945 EEEIQALTARDEIQKFDALRNSCTVITDLEEQNLQTEDEALNNOFPYLSKQJDEAS 1004
DB      961 EEEIQALTARDEIQKFDALRNSCTVITDLEEQNLQTEDEALNNOFPYLSKQJDEAS 1020
QY      1005 GANDEIVOLRSEVDHLRREITEREMQLTQOKTMEALTTCTMLEEQVMDLEALDELLE 1064
DB      1021 GANDEIVOLRSEVDHLRREITEREMQLTQOKTMEALTTCTMLEEQVMDLEALDELLE 1080
QY      1065 KERQWEAMRSVLDGSKQPEQCRVRELQMLDTEKQSRARADQRTESRQVVELAVKEHA 1124
DB      1081 KERQWEAMRSVLDGSKQPEQCRVRELQMLDTEKQSRARADQRTESRQVVELAVKEHA 1140
QY      1125 ELIALQALKEQKLEKASLSDKLANDLEKKHAMENNASLQOKLETRELEKORLLEQAK 1184
DB      1141 ELIALQALKEQKLEKASLSDKLANDLEKKHAMENNASLQOKLETRELEKORLLEQAK 1200
QY      1185 LQQQMDLOKNHIFRLTQGLQDALDADLLKTERSDLEYOLENIOVLYSHBEKYMEGTSIQ 1244
DB      1201 LQQQMDLOKNHIFRLTQGLQDALDADLLKTERSDLEYOLENIOVLYSHBEKYMEGTSIQ 1260
QY      1245 OTKLIDPLQAMWQAKKKKGLFSRKEDPALPVOVPLQVNEIKALKEKARCALEBA 1304
DB      1261 OTKLIDPLQAMWQAKKKKGLFSRKEDPALPVOVPLQVNEIKALKEKARCALEBA 1305
QY      1305 LQKTRIEIERSAREEAHRKATDHPSTPATARQOIAASAIYVSEBHPQPSAMSLAPSS 1364
DB      1306 LQKTRIEIERSAREEAHRKATDHPSTPATARQOIAASAIYVSEBHPQPSAMSLAPSS 1365
QY      1365 RKESSTPEBFSRRLKEBMHNHPIRRFVNGLMRATKCAVCLDLYHFSROASKLECOVM 1424
DB      1366 RKESSTPEBFSRRLKEBMHNHPIRRFVNGLMRATKCAVCLDLYHFSROASKLECOVM 1425
QY      1425 CHPKSTCLPATCGLPARYATHFEAFCDKDNNSGLQTKPSSSLHIGMMKVPRNKR 1484
DB      1426 CHPKSTCLPATCGLPARYATHFEAFCDKDNNSGLQTKPSSSLHIGMMKVPRNKR 1485
QY      1485 GQCGMDRKYIYLEGSKVLIYNNEAREAGQREVEBEELCLPDGDVSIHGAVGASELANTAK 1544
DB      1486 GQCGMDRKYIYLEGSKVLIYNNEAREAGQREVEBEELCLPDGDVSIHGAVGASELANTAK 1545
QY      1545 A-----EKABADAKL 1554
DB      1546 ADVPIILMESHPIITTCWPGRTLYLLAPSPDKORWYALLESVAVAGRVSEBKEADAKL 1605
QY      1555 LGSNLSKLJEGDRLDMNCTLPSPDOVVLVGREBGVYALNVLKNSLTHVPGVGAVFQIYI 1614
DB      1606 LGSNLSKLJEGDRLDMNCTLPSPDOVVLVGREBGVYALNVLKNSLTHVPGVGAVFQIYI 1665
QY      1615 KDLKELMIAGEERALCLVDYKVKOSILAQSHLPAQPDISPNIPEAVNGCHLFGAKLEN 1674
DB      1666 KDLKELMIAGEERALCLVDYKVKOSILAQSHLPAQPDISPNIPEAVNGCHLFGAKLEN 1725
QY      1675 GLCTCAMPKSVVILRYNENISKYCIKREIETSEPCSIHTNTNSILIGTKKFEIDMKQ 1734
DB      1726 GLCTCAMPKSVVILRYNENISKYCIKREIETSEPCSIHTNTNSILIGTKKFEIDMKQ 1785
QY      1735 YLLEEFIDKNHSLAPAFVASSNSFPVSIYQVNSAGQREBYLLCFHFGFVDSYGRS 1794
DB      1786 YLLEEFIDKNHSLAPAFVASSNSFPVSIYQVNSAGQREBYLLCFHFGFVDSYGRS 1845
QY      1795 RTDDLKWSRLPLAAYREPYLFTVHFNSLEVIETIQASSAGCTPARAYLDINPPYLGPAI 1854
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Db 1846 RTDCLKSRRLPLAFAYREPLYFTVTHFNSLEVIETIQASASGTPARAVLDIPNRYLGPAT 1905
 QY 1855 SSGAIYIASSYODKLRVYICCKGNLYKSSGTEHHRGPSTR 1894
 Db 1906 SSGAIYIASSYODKLRVYICCKGNLYKSSGTEHHRGPSTR 1945

RESULT 13

US-09-964-956-40
 ; Sequence 40, Application US/09964956
 ; Publication No. US20040043926A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gerlach, Valerie L
 ; APPLICANT: Macdougall, John R
 ; APPLICANT: Smithson, Glenda
 ; APPLICANT: Miller, Isabelle
 ; APPLICANT: Stone, David
 ; APPLICANT: Gunther, Erik
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Grose, William M
 ; APPLICANT: Alsbrook II, John P
 ; APPLICANT: Lepley, Denise M
 ; APPLICANT: Burgess, Catherine E
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Splet, Kimberly A
 ; APPLICANT: Leach, Martin D
 ; APPLICANT: Shinkete, Richard A
 ; TITLE OF INVENTION: No. US20040043926A1 Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-124
 ; CURRENT APPLICATION NUMBER: US/09/964,956
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: 60/235,631
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/235,633
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/235,808
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/236,064
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/236,065
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/236,066
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/236,135
 ; PRIOR FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: 60/237,434
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/238,321
 ; PRIOR FILING DATE: 2000-10-05
 ; PRIOR APPLICATION NUMBER: 60/238,399
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,396
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/276,667
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/294,823
 ; PRIOR FILING DATE: 2001-05-31
 ; PRIOR APPLICATION NUMBER: 60/304,868
 ; PRIOR FILING DATE: 2001-07-12
 ; NUMBER OF SEQ ID NOS: 127
 ; SOFTWARE: Patent Ver. 2.1
 ; SEQ ID NO 40
 ; LENGTH: 1641
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-964-956-40

Query Match 73.6%; Score 7717.5; DB 11; Length 1641;
 Best Local Similarity 90.8%; Pred. No. 0;
 Matches 1541; Conservative 15; Mismatches 16; Indels 125; Gaps 5;

QY 374 PFVPTLKSDDDTNSPFPEKNSWSSPQQLSPSGSGEELPFVGSYSKALGILGRSES 433

Db 1 PFVPTLKSDDDTNSPFPEKNSWSSVQQLSPSGSGEELPFVGSYSKALGILGRSES 60
 QY 434 VVSGLDSPAKTSMKKLLIKSKEIQDQDKCHMEQENTRLHRRVSEVAVLSQKEVEL 493
 Db 61 VVSSLDSPAKVSMKKLLIKSKEIQDQDKCHMEQENTRLHRRVSEVAVLSQKEVEL 120
 QY 494 KASETORSLLEODLAIYITECSLRSLEQARNEVSQEDDKLQQLHDI REQSRLQETK 553
 Db 121 KASETORSLLEODLAIYITECSLRSLEQARNEVSQEDDKLQQLHDI REQSRLQETK 180
 QY 554 EOEYQAVEEMRLMMNQLEEDLVASARRSDLYESLRESRLAAEFKRAECQHLTKA 613
 Db 181 EOEYQAVEEMRLMMNQLEEDLVASARRSDLYESLRESRLAAEFKRAECQHLTKA 240
 QY 614 KDQKPEVEGYATLEKINAEQQLKIQELQELKA-----AKERAEL 657
 Db 241 KDQKPEVEGYATLEKINAEQQLKIQELQELKA-----AKERAEL 300
 QY 658 EKLQNRDESEGRKLVAEERRHSLKVKRLTEMERENRKLDDIQTSQIQQMD 717
 Db 301 EKLNRDESEGRKLVAE----- 321
 QY 718 KILELEKREAVSAQHLEVHLKQEQHYEEKIKVLDNQIKKDLADKETLENMQRHE 777
 Db 322 ---ELEEKREAVSAQHLEVHLKQEQHYEEKIKVLDNQIKKDLADKETLENMQRHE 378
 QY 778 EAHKSKILSEQAMINAMDSKIRSLRIVELSEANKLAANSLEFQNRMAQEEWSE 837
 Db 379 EAHKSKILSEQAMINAMDSKIRSLRIVELSEANKLAANSLEFQNRMAQEEWSE 438
 QY 838 LRQOKRYLETQAKGLAQRKLEBEQLEKISHQDSKXNRLLEFTLRVSLHEEQKLE 897
 Db 439 LRQOKRYLETQAKGLAQRKLEBEQLEKISHQDSKXNRLLEFTLRVSLHEEQKLE 498
 QY 898 LRQOLTELQSLQERESQTLQAAAPALAESQLRQKTELEFTLAESEIQLTAHRDE 957
 Db 499 LRQOLTELQSLQERESQTLQAAAPALAESQLRQKTELEFTLAESEIQLTAHRDE 558
 QY 958 IORKEFDALNSCTVITDLEBQNLQTEDNAELNNQNFYLSKQLEASGANDEIVQLRSEV 1017
 Db 559 IORKEFDALNSCTVITDLEBQNLQTEDNAELNNQNFYLSKQLEASGANDEIVQLRSEV 618
 QY 1018 DILRRRITERMQLTSQKOTMBALKTTCMLSEQVMDLALDELLEKRWBAWRSVYG 1077
 Db 619 DILRRRITERMQLTSQKOTMBALKTTCMLSEQVMDLALDELLEKRWBAWRSVYG 678
 QY 1078 DEKSOPECHVRELQRLDTEKOSRABADQRTIESQVVELAVKHEKATILAQALKEOK 1137
 Db 679 DEKSOPECHVRELQRLDTEKOSRABADQRTIESQVVELAVKHEKATILAQALKEOK 738
 QY 1138 LVAESLSDKLNDLEKKHMLNNANSLQOKLETERBELKORLLEBQAKLQOQMDLQKNTIF 1197
 Db 739 LVAESLSDKLNDLEKKHMLNNANSLQOKLETERBELKORLLEBQAKLQOQMDLQKNTIF 798
 QY 1198 RLITQGLQELADPADLKTERSDLEYLENIQVLYSHEKRYMGTTISQOTKLIDFLQAKND 1257
 Db 799 RLITQGLQELADPADLKTERSDLEYLENIQVLYSHEKRYMGTTISQOTKLIDFLQAKND 858
 QY 1258 OPAKKKKGLFSRKEDPALPTQVPLQVNELKLALEKAKACALEBALQKTIELRSANE 1317
 Db 859 OPAKKKKGLFSRKEDPALPTQVPLQVNELKLALEKAKACALEBALQKTIELRSANE 903
 QY 1318 EAAHRKATDHPSPSPATARQOIAWSAIVRSPEHQPSANSLAPSSRRKESSTPEEFGR 1377
 Db 904 EAAHRKATDHPSPSPATARQOIAWSAIVRSPEHQPSANSLAPSSRRKESSTPEEFGR 963
 QY 1378 RLKERMENHNIPIHRENVGLMRAATKCAVCLDPTHFGROASKLECYVMCHPKSTCLPATC 1437
 Db 964 RLKERMENHNIPIHRENVGLMRAATKCAVCLDPTHFGROASKLECYVMCHPKSTCLPATC 1023
 QY 1438 GLPAEYATHTFAFRDKNNSPGLQTKPESSSLHLEGMKVRNNKRGQGGDRKYTYVE 1497

Db 1024 GLPAEYATHPTFAFCRDKNNSPGLQSKPESSSLHLEGMMKVPNNRNGGQMDRKXIVLE 1083
Qy 1498 GSGVLIYDNEARAGORPVEBEFELCLPDGDSVTHGAVGASELANATAKA----- 1545
Db 1084 GSKVLIYDNEARAGORPVEBEFELCLPDGDSVTHGAVGASELANATAKAVPYILKMSHP 1143
Qy 1546 -----EKAEDATLGNLSILKLEGGDR 1567
Db 1144 HTTCWGRRLIYLLAPSPDKORWTVLSEVVAGGARSREKAEADAKLGNLSLKEGGDR 1203
Qy 1568 LDMNCTLPFSDQVYLVGTEBGLYALNVLNKSLTHVPGIGAVFOIYIILKOLEKLMTAGEE 1627
Db 1204 LDMNCTLPFSDQVYLVGTEBGLYALNVLNKSLTHVPGIGAVFOIYIILKOLEKLMTAGEE 1263
Qy 1628 PALCLVDYKVKQSLAQSHLPAPDIPSPVFEAVKCGHLPAGKINGLCICAMPSTKV 1687
Db 1264 PALCLVDYKVKQSLAQSHLPAPDIPSPVFEAVKCGHLPAGKINGLCICAMPSTKV 1323
Qy 1688 IIRYENLSKYCIKREIETSEPCSCIHFTNYSILIGTNKFYEIDMKQYTLLEFLDKNDHS 1747
Db 1324 IIRYENLSKYCIKREIETSEPCSCIHFTNYSILIGTNKFYEIDMKQYTLLEFLDKNDHS 1383
Qy 1748 LAPAVFASSNSFPVSIYVNSAGQREYLLCFHEGFVDSYGRSRTDCLKMSRLPLA 1807
Db 1384 LAPAVFASSNSFPVSIYVNSAGQREYLLCFHEGFVDSYGRSRTDCLKMSRLPLA 1443
Qy 1808 FAYREYLLFVTHPNSLEVEIEIQARSSAGTPARAYLIDIPNRYLGPRISSGAIYLAASYD 1867
Db 1444 FAYREYLLFVTHPNSLEVEIEIQARSSAGTPARAYLIDIPNRYLGPRISSGAIYLAASYD 1503
Qy 1868 KLRVICCKGNLVKSGTEHHRGCPSTSSPNKRGPTYNEHITKRVASSPAPPEGSHPR 1927
Db 1504 KLRVICCKGNLVKSGTEHHRGCPSTSSPNKRGPTYNEHITKRVASSPAPPEGSHPR 1563
Qy 1928 EPSTPHRY--REGRTFLRDKSPGRPLERKSPGRMLSTRRSPGRLEFEDSSRGRLPAG 1985
Db 1564 EPSTPHRYRDRGRGRTFLRDKSPGRPLERKSPGRMLSTRRSPGRLEFEDSSRGRLPAG 1623
Qy 1986 AVRTPLSQVNGKRGQSA 2002
Db 1624 AVRTPLSQVNGKRWQDSS 1640

RESULT 14
US-10-017-216-5
; Sequence 5, Application US/10017216
; Publication No. US20020160483A1
; GENERAL INFORMATION:
; APPLICANT: KAPTELER-LIBERMANN, Rosana
; TITLE OF INVENTION: 13245, A No. US20020160483A1el Human Myotonic Dystrophy Type Prot
; FILE REFERENCE: 10147-57U1
; CURRENT APPLICATION NUMBER: US/10/017, 216
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/242, 429
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1641
; TYPE: PRF
; ORGANISM: Mus musculus
US-10-017-216-5

Query Match 73.6%; Score 7717.5; DB 13; Length 1641;
Best Local Similarity 90.8%; Pred. No. 0;
Matches 1441; Conservative 15; Mismatches 16; Indels 125; Gaps 5;

Qy 374 PEVPTLKSDDDTSNPEPEKNSWSSPCQLSPSGSGEELPFVGSYSKALGIIIGRSRS 433
Db 1 PEVPTLKSDDDTSNPEPEKNSWSSPCQLSPSGSGEELPFVGSYSKALGIIIGRSRS 60
Qy 434 VVSGLDSPAKTSSMEKKLLIKSEKIQDSQDKHMEQENTRLHRRVSEVAVLQKEVEL 493

Db 61 VVSGLDSPAKTSSMEKKLLIKSEKIQDSQDKHMEQENTRLHRRVSEVAVLQKEVEL 120
Qy 494 KASRTORSLEBDLATYITTECSLKRSLSEQAMEVSOEDDKALQLLHDIREGSRKLQIBX 553
Db 121 KASRTORSLEBDLATYITTECSLKRSLSEQAMEVSOEDDKALQLLHDIREGSRKLQIBX 180
Qy 554 EOEYQAOVBEMLMNNOLEBEDVVSARRSDLYESLRSRLAEEFKKATRCQKLLKA 613
Db 181 EOEYQAOVBEMLMNNOLEBEDVVSARRSDLYESLRSRLAEEFKKATRCQKLLKA 240
Qy 614 KOQKPEVGEYAKLEKINABOOLKIQEOLKEKLEA-----AKESAEREL 657
Db 241 KOQKPEVGEYAKLEKINABOOLKIQEOLKEKLEA-----AKESAEREL 300
Qy 658 EKLQNRSDSEGIKKVLEAEERRRSLNNKVRLEBTMERRENLMDIQTSQOIQOMAD 717
Db 301 EKLQNRSDSEGIKKVLEAE----- 321
Qy 718 KLELEKREKREAOVAOHLFVHLKQEQHYEKIYVLDNOIKQIADKETELENMQRHE 777
Db 322 ---ELBEKREAOVAOHLFVHLKQEQHYEKIYVLDNOIKQIADKETELENMQRHE 378
Qy 778 EAHKRGKILSEOKAMINAMDSKIRSLBORIYELSEANKLAANSLEPTORNMKAQEMTISE 837
Db 379 EAHKRGKILSEOKAMINAMDSKIRSLBORIYELSEANKLAANSLEPTORNMKAQEMTISE 438
Qy 838 LRQKPYLETQAGKLEAONRKLEBQLEKI SHQDSKRNRLLELTRLEVSLEHEQKLE 897
Db 439 LRQKPYLETQAGKLEAONRKLEBQLEKISHQDSKRNRLLELTRLEVSLEHEQKLE 498
Qy 898 LKROLTELQLOEESQUTALQARALLESOLRAKTELETTAEAREEQAALTANDE 957
Db 499 LKROLTELQLOEESQUTALQARALLESOLRAKTELETTAEAREEQAALTANDE 558
Qy 958 IQRKFDALRNSCTVITDLEBOLNQLTEDNAEINNOFYLSKQIDBASGANDIYOLARSEV 1017
Db 559 IQRKFDALRNSCTVITDLEBOLNQLTEDNAEINNOFYLSKQIDBASGANDIYOLARSEV 618
Qy 1018 DILREITEREMOULTSOKQMEALKTCTMLBEQVMDLEALNDEILEKROMEANRSYLG 1077
Db 619 DILREITEREMOULTSOKQMEALKTCTMLBEQVMDLEALNDEILEKROMEANRSYLG 678
Qy 1078 DEKSOFEGRVLELOMULTEKOSRARADORTTESOVVLELVKHEKATILALQOLKXOK 1137
Db 679 DEKSOFEGRVLELOMULTEKOSRARADORTTESOVVLELVKHEKATILALQOLKXOK 738
Qy 1138 LKASLSDKLNDLEKHAMLEMNARSLOOKLETERELKORLLEBQAKIQOQMDLOKNHIF 1197
Db 739 LKASLSDKLNDLEKHAMLEMNARSLOOKLETERELKORLLEBQAKIQOQMDLOKNHIF 798
Qy 1198 RLTQGLQALDRAIDLKTERSDLEYOLENIOVLYSHEKVKMEGTISQOTKLDIFQATMD 1257
Db 799 RLTQGLQALDRAIDLKTERSDLEYOLENIOVLYSHEKVKMEGTISQOTKLDIFQATMD 858
Qy 1258 OPAKKKKGLFSRRKEDPALPTPOVPLQVNEKLALKEKARCALEALOKRIEIRSAE 1317
Db 859 OPAKKKK-----VPLQVNEKLALKEKARCALEALOKRIEIRSAE 903
Qy 1318 EAAHKKATDHPHSTPATARQOIASAIVRSPEHQPSAMSLAPPSRRKSSSTPEBSR 1377
Db 904 EAAHKKATDHPHSTPATARQOIASAIVRSPEHQPSAMSLAPPSRRKSSSTPEBSR 963
Qy 1378 RLKERMHNNIIPRRVNGAMRATKCAVCLDVHGRQASKLEJCQVMCHPCKSTCLPATYC 1437
Db 964 RLKERMHNNIIPRRVNGAMRATKCAVCLDVHGRQASKLEJCQVMCHPCKSTCLPATYC 1023
Qy 1438 GLPAEYATHPTFAFCRDKNNSPGLQSKPESSSLHLEGMMKVPNNRNGGQMDRKXIVLE 1497
Db 1024 GLPAEYATHPTFAFCRDKNNSPGLQSKPESSSLHLEGMMKVPNNRNGGQMDRKXIVLE 1083
Qy 1498 GSKVLIYDNEARAGORPVEBEFELCLPDGDSVTHGAVGASELANATAKA----- 1545

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Db      1084 GSKYLLYDNEAREAGORPVEEFELCLPDGDSIHGAVGASELANTAKADVPIILKMSHP 1143
Qy      1546 -----EKAEDATLNGSLKLEGGDR 1567
Db      1144 HTTCMPGRLLYLLAFSPDKQWVTALESVAVAGRVAREADAKLGLSLKLEGGDR 1203
Qy      1568 LDMNCTLPSPDQVVLVGTBEGLYALNVLKSLTHVPGIGAVFOIYIILKDEKLMTAGEE 1627
Db      1204 LDMNCTLPSPDQVVLVGTBEGLYALNVLKSLTHVPGIGAVFOIYIILKDEKLMTAGEE 1263
Qy      1628 RALCLVDVKKVKSQSLAQSHLPAQPDISPNIFFAVKGCHEFGAGKIENGLICICAMPSPKV 1687
Db      1264 RALCLVDVKKVKSQSLAQSHLPAQPDISPNIFFAVKGCHEFGAGKIENGLICICAMPSPKV 1323
Qy      1688 ILRYNNTLSKYCKRKIEIETSEPCSHFTMYSLILGINKYEIDMQYTLDEFLDKNDHS 1747
Db      1324 ILRYNNTLSKYCKRKIEIETSEPCSHFTMYSLILGINKYEIDMQYTLDEFLDKNDHS 1383
Qy      1748 LAPAVFAASNSFPVSIIVQVNSAGOREBYLLCFHEFGVFDYSYGRSRITDCLKMSRLPLA 1807
Db      1384 LAPAVFAASNSFPVSIIVQVNSAGOREBYLLCFHEFGVFDYSYGRSRITDCLKMSRLPLA 1443
Qy      1808 FAYREBYLFTVTHNSLEVIIEIQARSSAGTPARAYLDPNPRYLGPALISSGAIYLAASYOD 1867
Db      1444 FAYREBYLFTVTHNSLEVIIEIQARSSAGTPARAYLDPNPRYLGPALISSGAIYLAASYOD 1503
Qy      1868 KLRVITCKGNLVESGTEHHRGSTRSSPNKRGPTVYHHTIKRVAASSAPPEGSHR 1927
Db      1504 KLRVITCKGNLVESGTEHHRGSTRSSPNKRGPTVYHHTIKRVAASSAPPEGSHR 1563
Qy      1928 EPSTPHRY--REGRTELRDKSPGRPLERKSPGRMLSTRERSPGRLPFEDSRGRPLPG 1985
Db      1564 EPSTPHRYRDRERTELRDKSPGRPLERKSPGRMLSTRERSPGRLPFEDSRGRPLPG 1623
Qy      1986 AVRTPLSQVNRKGQGA 2002
Db      1624 AVRTPLSQVNRKWDQSS 1640

RESULT 15
US-09-964-956-41
; Sequence 41, Application US/09964956
; Publication No. US20040043926A1
; GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Grobse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine B
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Kekuda, Kamesh
; APPLICANT: Szytek, Kimberly A
; APPLICANT: Leach, Martin D
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20040043926A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-124
; CURRENT APPLICATION NUMBER: US/09/964,956
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,631
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,633
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,808
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,064
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; PRIOR APPLICATION NUMBER: 60/236,135
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,434
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,399
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; PRIOR APPLICATION NUMBER: 60/276,667
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/294,823
; PRIOR FILING DATE: 2001-05-31
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; PRIOR FILING DATE: 2001-07-12
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; ORGANISM: Mus musculus
US-09-964-956-41

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GenCore version 5.1.6
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Searched: 5401638 seqs, 2966923429 residues

Total number of hits satisfying chosen parameters: 10803276

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8	5661.4	91.9	6165	US-10-791-666-1	Sequence 1, Appl1
9	5651.8	91.8	8656	US-10-618-941-1	Sequence 1, Appl1
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44	230.4	3.7	4917	US-10-796-177-121	Sequence 121, App
45	228.2	3.7	2785	US-10-172-118-930	Sequence 930, App

ALIGNMENTS

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Sequence 3, Application US/10017216				
Publication No. US20020160483A1				
GENERAL INFORMATION:				
APPLICANT: KAPILLER-LIBERMANN, Rosana				
TITLE OF INVENTION: 13245, A No. US20020160483A1e1 Human Myotonic Dystrophy Type Pro				
TITLE OF INVENTION: Kinase and Uses Therefor				
FILE REFERENCE: 10147-57U1				
CURRENT APPLICATION NUMBER: US/10/017,216				
CURRENT FILING DATE: 2001-10-23				
PRIOR APPLICATION NUMBER: US 60/242,429				
PRIOR FILING DATE: 2000-10-23				
NUMBER OF SEQ ID NOS: 7				
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DB 2581 GAGCAGCTGAGAAAGATCAGCCACCAAGACCAAGACCAAGATGCGCTGTGAACTG 2640
QY 2641 GAGACAAAGATTGCGGAGGTCACTTAGACAGAGGACAGAACTGGAGCTCAAGCGC 2700
DB 2641 GAGACAAAGATTGCGGAGGTCACTTAGACAGAGGACAGAACTGGAGCTCAAGCGC 2700
QY 2701 CAGCTCAAGAGCTTACAGCTCTCTCTGACAGAGCGGAGTCAAGTTGACAGCCCTGAC 2760
DB 2701 CAGCTCAAGAGCTTACAGCTCTCTCTGACAGAGCGGAGTCAAGTTGACAGCCCTGAC 2760
QY 2761 GCTGACGCGGCGCCTGAGAGCAAGCTTCCGACAGGCAAGACAGAGCTGAAAGAC 2820
DB 2761 GCTGACGCGGCGCCTGAGAGCAAGCTTCCGACAGGCAAGACAGAGCTGAAAGAC 2820
QY 2821 ACAGCAAGAGCTGAGAGAGATCCAGCACTCAGCGCACTAGAGATGAAATCCAGCGC 2880
DB 2821 ACAGCAAGAGCTGAGAGAGATCCAGCACTCAGCGCACTAGAGATGAAATCCAGCGC 2880
QY 2881 AAATTTGATGCTTTCTGTATCAGCTGTATCTGTATATCAGACCTTGAAGAGAGCTTAAC 2940
DB 2881 AAATTTGATGCTTTCTGTATCAGCTGTATCTGTATATCAGACCTTGAAGAGAGCTTAAC 2940
QY 2941 CAGCTGACGAGACCAAGCTGAATCAACCAACAAATCTTACTTGTCAACCAACTC 3000
DB 2941 CAGCTGACGAGACCAAGCTGAATCAACCAACAAATCTTACTTGTCAACCAACTC 3000
QY 3001 GATGAGGCTTCTGCGCCCAACGACGAGATTGTACAACTGGAAGTGAAGCAATCTC 3060
DB 3001 GATGAGGCTTCTGCGCCCAACGACGAGATTGTACAACTGGAAGTGAAGCAATCTC 3060
QY 3061 CCGCGGAGATCAACGAGACGAGATGCAAGCTTACCGCAGAGCAAGAGATGAGGCT 3120
DB 3061 CCGCGGAGATCAACGAGACGAGATGCAAGCTTACCGCAGAGCAAGAGATGAGGCT 3120
QY 3121 CTGAAGACCAAGTCAACATGCTGAGAGAAACAGTCAATGATTTGAGAGCCCTAAACGAT 3180
DB 3121 CTGAAGACCAAGTCAACATGCTGAGAGAAACAGTCAATGATTTGAGAGCCCTAAACGAT 3180
QY 3181 GAGCTGTAAGAAAGAGCGGAGTGGAGGCTTGAAGAGCGTCTGAGTGAAGAA 3240
DB 3181 GAGCTGTAAGAAAGAGCGGAGTGGAGGCTTGAAGAGCGTCTGAGTGAAGAA 3240
QY 3241 TCCCAAGTTGAGTGTGGGTTGAGAGCTGAGAGAAATGCTGACACCGAGAAACAGAGC 3300
DB 3241 TCCCAAGTTGAGTGTGGGTTGAGAGCTGAGAGAAATGCTGACACCGAGAAACAGAGC 3300
QY 3301 AGGCGAGAGCCGATCAGCGGATCAACGAGTCTCCGAGGTGGAGCTGGAGAG 3360
DB 3301 AGGCGAGAGCCGATCAGCGGATCAACGAGTCTCCGAGGTGGAGCTGGAGAG 3360
QY 3361 GAGCAAAAGCTGAGATTTCTGCTGACAGAGGCTTCAAGAGCAAGAGCTGAAGGCC 3420
DB 3361 GAGCAAAAGCTGAGATTTCTGCTGACAGAGGCTTCAAGAGCAAGAGCTGAAGGCC 3420

QY 3421 GAGAGCTCTGACAAAGCTCAATGACCTGAGAAAGACATGCTATGCTTGAATGAAT 3480
DB 3421 GAGAGCTCTGACAAAGCTCAATGACCTGAGAAAGACATGCTATGCTTGAATGAAT 3480
QY 3481 GCCCGAGCTTACAGCAAGAGCTGAGAGCTGAACGAGAGCTCAACAGAGCTTCTGAA 3540
DB 3481 GCCCGAGCTTACAGCAAGAGCTGAGAGCTGAACGAGAGCTCAACAGAGCTTCTGAA 3540
QY 3541 GAGCAAGCCAAATTAACAGAGAGATGAGCTGCGAGAAATCAATTTTCCGTGAGCT 3600
DB 3541 GAGCAAGCCAAATTAACAGAGAGATGAGCTGCGAGAAATCAATTTTCCGTGAGCT 3600
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DB 3601 CAAGAGCTCAAGAGCTTATGATCGGCTGATCTTACTGAAGACAGAAAGAGTGACTTG 3660
QY 3661 GAGTATCAGCTGAGAAACATTCAGGTTCTATTTCTCATGAAAGGTGAAATGAGAGC 3720
DB 3661 GAGTATCAGCTGAGAAACATTCAGGTTCTATTTCTCATGAAAGGTGAAATGAGAGC 3720
QY 3721 ACTATTTCTCAACAAACCAACTCATGATTTTCTGCAAGCCAAATGAGCAACCTGCT 3780
DB 3721 ACTATTTCTCAACAAACCAACTCATGATTTTCTGCAAGCCAAATGAGCAACCTGCT 3780
QY 3781 AAAAAGAAAAAGGTTTATTTAGTGAACGAAAGAGAACCTGCTTACCAACAGATT 3840
DB 3781 AAAAAGAAAAAGGTTTATTTAGTGAACGAAAGAGAACCTGCTTACCAACAGATT 3840
QY 3841 CCTCTGACATGATGATGAGTGAAGCTGCGCTGAGAGAGAGAAAGCTGCTGTGAGAG 3900
DB 3841 CCTCTGACATGATGATGAGTGAAGCTGCGCTGAGAGAGAGAAAGCTGCTGTGAGAG 3900
QY 3901 CTGAGAGAGGCTTCTGAGAGACCCGATCTGAGCTCCGCTCCGCGGAGAGAGAGTGC 3960
DB 3901 CTGAGAGAGGCTTCTGAGAGACCCGATCTGAGCTCCGCTCCGCGGAGAGAGAGTGC 3960
QY 3961 CACCGCAAGACCAAGGACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 4020
DB 3961 CACCGCAAGACCAAGGACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 4020
QY 4021 GCCATGTCGCAATCGTGGGTCGCGAGAGACCAAGCCAGTGCATGAGCTGCTGCC 4080
DB 4021 GCCATGTCGCAATCGTGGGTCGCGAGAGACCAAGCCAGTGCATGAGCTGCTGCC 4080
QY 4081 CCGCATTCAGCGCGAGAAAGAGTCTTCACTCCAGAGAAATTTAGTGGGCTTTAAG 4140
DB 4081 CCGCATTCAGCGCGAGAAAGAGTCTTCACTCCAGAGAAATTTAGTGGGCTTTAAG 4140
QY 4141 GAAAGCATGACCAATTAATCTCTCAACGATTCAGCTGAGACTGAACATGCGAGCACA 4200
DB 4141 GAAAGCATGACCAATTAATCTCTCAACGATTCAGCTGAGACTGAACATGCGAGCACA 4200
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DB 4201 AAGTGTCTGTGTCTGTGATACCGTGAACCGTGAACCGCAGAGATCCAAATGCTCGAA 4260
QY 4261 TGTCAAGTATGTGTCAACCCCAAGTGTCTCAAGTGTCTTCCAGCCCTGCGGCTTGC 4320
DB 4261 TGTCAAGTATGTGTCAACCCCAAGTGTCTCAAGTGTCTTCCAGCCCTGCGGCTTGC 4320
QY 4321 GCTGAATATGCAACATTCACCGAGGCTTCTGCGTGAACAAATGAATCCCAAGT 4380
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QY 4381 CTCGACCAAGAGGCTGAGAGCTTGAACCTTGAAGAGGTGAAGGTGCCAG 4440
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QY 4441 AATTAACAAAGAGACAGCAAGGCTTGAACAGAAATATCTTCTGAGAGGATTAATA 4500
DB 4441 AATTAACAAAGAGACAGCAAGGCTTGAACAGAAATATCTTCTGAGAGGATTAATA 4500
QY 4501 GTCCTATTATATGCAATGAGACCAAGAAAGCTGACAGAGGCGGTGAAAGATTTGAG 4560

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Db      4501 GTCTCATTTATGACATGTAAGCCAGAGAGCTGACAGAGCCGGTGAAGATTTTGAG 4560
Qy      4561 CTGTGCTCTCCGACGGGAGTATCTTATTCATGTGCGGTGTGTTCCGAATCCGAC 4620
Db      4561 CTGTGCTCTCCGACGGGAGTATCTTATTCATGTGCGGTGTGTTCCGAATCCGAC 4620
Qy      4621 AATACAGCCAAAGCAAGAAAAAGCAAGCTGATGCTTAAATCTGTTGGAAAATCTCCCTGCTG 4680
Db      4621 AATACAGCCAAAGCAAGAAAAAGCAAGCTGATGCTTAAATCTGTTGGAAAATCTCCCTGCTG 4680
Qy      4681 AAACTGGAAGGTATGACCGTCTAGACATGAACTGACCGTGCCTTCAGTGCAGAGTG 4740
Db      4681 AAACTGGAAGGTATGACCGTCTAGACATGAACTGACCGTGCCTTCAGTGCAGAGTG 4740
Qy      4741 GTGTGTGTGGGACCCGAGAGAGGGCTCTAGCCCTGAATGTCTTAAAAATCTCCCTAAC 4800
Db      4741 GTGTGTGTGGGACCCGAGAGAGGGCTCTAGCCCTGAATGTCTTAAAAATCTCCCTAAC 4800
Qy      4801 CATGTCCAGGAATTGAGAGCTTCCAAATTTATATTAACAAGGACCTGAGAGACTTA 4860
Db      4801 CATGTCCAGGAATTGAGAGCTTCCAAATTTATATTAACAAGGACCTGAGAGACTTA 4860
Qy      4861 CTCATGATAGCAGAGAGAGAGCGGCACTGTGTCTTGTGGAAGTGAAGAAAGTGAACAG 4920
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Qy      4921 TCCCTGGCCCAAGTCCCACTGCTGCCACGCCGACATCTCACCCAACTTTTGAAGCT 4980
Db      4921 TCCCTGGCCCAAGTCCCACTGCTGCCACGCCGACATCTCACCCAACTTTTGAAGCT 4980
Qy      4981 GTCAAGGGCTGCCACTTGTGTGGGAGGAGCAAGATTGAGAGCGGGCTCGCATGTGTGA 5040
Db      4981 GTCAAGGGCTGCCACTTGTGTGGGAGGAGCAAGATTGAGAGCGGGCTCGCATGTGTGA 5040
Qy      5041 GCCATGCCAGCAAAAGTGTCTATCTCGGCTACCAAGAAACCTCAGCAATATCTGCATC 5100
Db      5041 GCCATGCCAGCAAAAGTGTCTATCTCGGCTACCAAGAAACCTCAGCAATATCTGCATC 5100
Qy      5101 CGGAAAGAGATGAGAGCTTCAGAGCCCTGACAGCTGTATTCACCTTACCAATTAACGATTC 5160
Db      5101 CGGAAAGAGATGAGAGCTTCAGAGCCCTGACAGCTGTATTCACCTTACCAATTAACGATTC 5160
Qy      5161 CTCATTTGAACCAATTAATTTCTACGAATTCAGATGACATGAAACAGTACACGCTCGAGAAATTC 5220
Db      5161 CTCATTTGAACCAATTAATTTCTACGAATTCAGATGACATGAAACAGTACACGCTCGAGAAATTC 5220
Qy      5221 CTGGAATGAATGACCATTCCTTGGCACTGCTGTGTGTTGCGGCTCTTCCAAACAGCTTC 5280
Db      5221 CTGGAATGAATGACCATTCCTTGGCACTGCTGTGTGTTGCGGCTCTTCCAAACAGCTTC 5280
Qy      5281 CCTGTCTCAATCGTGAAGGTGAACAGCGAGGGGCGGAGAGAGTACTGTGTGTTC 5340
Db      5281 CCTGTCTCAATCGTGAAGGTGAACAGCGAGGGGCGGAGAGAGTACTGTGTGTTC 5340
Qy      5341 CACGAATTTGAGAGTGTCTGTGATTTCTTACGGAAGAGTGAAGCGGACAGATCTCAAG 5400
Db      5341 CACGAATTTGAGAGTGTCTGTGATTTCTTACGGAAGAGTGAAGCGGACAGATCTCAAG 5400
Qy      5401 TGGAGTCTGCTTACCTTTGGCTTTGCTTACAGAGAAACCTTATCTGTTGTGACCACTTC 5460
Db      5401 TGGAGTCTGCTTACCTTTGGCTTTGCTTACAGAGAAACCTTATCTGTTGTGACCACTTC 5460
Qy      5461 AACTCACTGAGATGATGATGATCCAGGAGCGCTCTCAGAGGGGACCCCTGCGGAGCG 5520
Db      5461 AACTCACTGAGATGATGATGATCCAGGAGCGCTCTCAGAGGGGACCCCTGCGGAGCG 5520
Qy      5521 TACCTGAGATCCGAAACCGGCTTACCTGTGGCCTTGCATTTCTTCAAGAGCATTTAC 5580
Db      5521 TACCTGAGATCCGAAACCGGCTTACCTGTGGCCTTGCATTTCTTCAAGAGCATTTAC 5580
Qy      5581 TTGGGTCTCTATACCAAGATTAATTAAGGCTCATTTGTGTCAGAGGAAACCTGCTGAAG 5640
Db      5581 TTGGGTCTCTATACCAAGATTAATTAAGGCTCATTTGTGTCAGAGGAAACCTGCTGAAG 5640
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Db      5581 TTGGGTCTCTATACCAAGATTAATTAAGGCTCATTTGTGTCAGAGGAAACCTGCTGAAG 5640
Qy      5641 GAGTCCGACATGAACACACACCGGGGCGCTGTCACCTCCGAGAGGCCCAACAGCGA 5700
Db      5641 GAGTCCGACATGAACACACACCGGGGCGCTGTCACCTCCGAGAGGCCCAACAGCGA 5700
Qy      5701 GGCCTCACCGTATCAAGAGCATTCACCAAGCGGTGGCTTCCAGCCAGCCGCC 5760
Db      5701 GGCCTCACCGTATCAAGAGCATTCACCAAGCGGTGGCTTCCAGCCAGCCGCC 5760
Qy      5761 GAAAGGCCAGCCACCGGAGAGGCAAGCACCCGCTTACCGGAGGGGGGAGCC 5820
Db      5761 GAAAGGCCAGCCACCGGAGAGGCAAGCACCCGCTTACCGGAGGGGGGAGCC 5820
Qy      5821 GAGTCCGACGAGCAAGTCTTCTGCGCGCCCTGAGAGGAGAAAGTCCCCGGCCGG 5880
Db      5821 GAGTCCGACGAGCAAGTCTTCTGCGCGCCCTGAGAGGAGAAAGTCCCCGGCCGG 5880
Qy      5881 ATGCTACAGCAGCGGAGAGAGCGGTCCCGGAGAGGCTGTTGAACAAGCAGCGGCG 5940
Db      5881 ATGCTACAGCAGCGGAGAGAGCGGTCCCGGAGAGGCTGTTGAACAAGCAGCGGCG 5940
Qy      5941 CGGCTGCTGCGGAGCGGTGAGAGACCCGCTGTCCAGGTGAACAAGAGAGGCGAG 6000
Db      5941 CGGCTGCTGCGGAGCGGTGAGAGACCCGCTGTGTCCAGGTGAACAAGAGAGGCGAG 6000
Qy      6001 AGTGCCTCTCAAGTTTACGGTTTAACTGTACCTATTAATGACTGGAATTAAGTCTG 6060
Db      6001 AGTGCCTCTCAAGTTTACGGTTTAACTGTACCTATTAATGACTGGAATTAAGTCTG 6060
Qy      6061 GACAACTGCGACGCTTACCTGTGAGTCTGTGAGATCACTCCGTAATGAGAGAAATCCGG 6120
Db      6061 GACAACTGCGACGCTTACCTGTGAGTCTGTGAGATCACTCCGTAATGAGAGAAATCCGG 6120
Qy      6121 CAGCAGTTGAAAGTCTGTCTGAGAACAGATTAATTC 6159
Db      6121 CAGCAGTTGAAAGTCTGTCTGAGAACAGATTAATTC 6159

RESULT 2
US-10-325-430-11
; Sequence 11, Application US/10325430
; Publication No. US20030153525A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Siles-Santiago, Immaculada
; APPLICANT: Rosenfeld, Julie Beth
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
; FILE REFERENCE: Mpi01-294PIRM
; CURRENT APPLICATION NUMBER: US/10/325,430
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/341,953
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6162
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(6162)
US-10-325-430-11

Query Match      100.0%; Score 6159; DB 16; Length 6162;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ATGTTGAAGTTCAAAATATGAGCGCGGAATCTTTGATGCTGTGTCTGAACCATTT 60
Db      1 ATGTTGAAGTTCAAAATATGAGCGCGGAATCTTTGATGCTGTGTCTGAACCATTT 60
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QY	61	GCACGCGGGGCTCCAGGCTAACTGTTCTTCCAGGGGAAACAACCCCTTATGACTCA	120
DB	61	GCACGCCGGGCTCCAGGCTAACTGTTCTTCCAGGGGAAACAACCCCTTATGACTCA	120
QY	121	CAGCAGATGTCTCCTCTTTCGAGAAAGGATATTAGATGCCCTCTTGTCTCTTGAA	180
DB	121	CAGCAGATGTCTCCTCTTTCGAGAAAGGATATTAGATGCCCTCTTGTCTCTTGAA	180
QY	181	GAATGCATCAGCCCTGCTCTGATGAAGTTTAAGCACTGACCACTTTGTCCGGAAGAT	240
DB	181	GAATGCATCAGCCCTGCTCTGATGAAGTTTAAGCACTGACCACTTTGTCCGGAAGAT	240
QY	241	TCCGACACCATAGCTGAGTTACAGAGGCTCCAGCCTTGCGAAAGAGCTTCCAAAGTCAG	300
DB	241	TCCGACACCATAGCTGAGTTACAGAGGCTCCAGCCTTGCGAAAGAGCTTCCAAAGTCAG	300
QY	301	AGCTCTTAGGTTGTGATCACTTGTCTGAAGTCAGAGTGSTPAAGAGAAAGCAACGGG	360
DB	301	AGCTCTTAGGTTGTGATCACTTGTCTGAAGTCAGAGTGSTPAAGAGAAAGCAACGGG	360
QY	361	GACATCTATGCTATGAAGAATGAAGAAGGCTTTATTTGGCCACGAGACAGATTCA	420
DB	361	GACATCTATGCTATGAAGAATGAAGAAGGCTTTATTTGGCCACGAGACAGATTCA	420
QY	421	TTTTTTGAGAAAGCGGAGACATATTATCTCGAAGCACAGCCCGTGATCCCCAATTA	480
DB	421	TTTTTTGAGAAAGCGGAGACATATTATCTCGAAGCACAGCCCGTGATCCCCAATTA	480
QY	481	CAGTATGCCCTTTCAGAGCAAAAATCACTTTATCTGATGAGAAATACAGCTTGAGGG	540
DB	481	CAGTATGCCCTTTCAGAGCAAAAATCACTTTATCTGATGAGAAATACAGCTTGAGGG	540
QY	541	GACTTGCTGTCACTTTTGATAGATATAGAGGACCGTAGTAGATGAAGAACTTGATCAAGTT	600
DB	541	GACTTGCTGTCACTTTTGATAGATATAGAGGACCGTAGTAGATGAAGAACTTGATCAAGTT	600
QY	601	TAGCTAGCTGAGCTGATTTTGGCTGTTCACAGCCTTCATCTGATGGATACGTGCATCGA	660
DB	601	TAGCTAGCTGAGCTGATTTTGGCTGTTCACAGCCTTCATCTGATGGATACGTGCATCGA	660
QY	661	GACATCAAGCCCTGAGAAATCTGTGTAACCGGACAGGACATCAACAGCTGTGATTTT	720
DB	661	GACATCAAGCCCTGAGAAATCTGTGTAACCGGACAGGACATCAACAGCTGTGATTTT	720
QY	721	GGATCTGCGCGAAATGATTCACAACAAGATGTGAATGCCAACTCCGATTTGGGACC	780
DB	721	GGATCTGCGCGAAATGATTCACAACAAGATGTGAATGCCAACTCCGATTTGGGACC	780
QY	781	CCAGATTACATGAGCTCTGAAAGTGCTGACTGTATGAACGGGAGATGGAAGGACCTTAC	840
DB	781	CCAGATTACATGAGCTCTGAAAGTGCTGACTGTATGAACGGGAGATGGAAGGACCTTAC	840
QY	841	GGCCCTGAGCTGATGAGTGTGAGTGGGCGGATGTGCTATGATGATGATTTATGGGAGA	900
DB	841	GGCCCTGAGCTGATGAGTGTGAGTGGGCGGATGTGCTATGATGATGATTTATGGGAGA	900
QY	901	TCCCCCTTTCGAGAGGAACTCTGACCAAACTTCAATTAACATTATGAAATTTCCAGCG	960
DB	901	TCCCCCTTTCGAGAGGAACTCTGACCAAACTTCAATTAACATTATGAAATTTCCAGCG	960
QY	961	TTTTTGAATTTCCAGATGACCCCAAGATGACGATGACTTCTTGAATCTGATTCACAAAGC	1020
DB	961	TTTTTGAATTTCCAGATGACCCCAAGATGACGATGACTTCTTGAATCTGATTCACAAAGC	1020
QY	1021	TTGTGTGCGGCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGTGCTCATCTTTCTTC	1080
DB	1021	TTGTGTGCGGCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGTGCTCATCTTTCTTC	1080
QY	1081	TCATAAATTGACTGGAACAACATTGTGTACTCTCTCCCTCTTGTGTTCCACCTCAAG	1140
DB	1081	TCATAAATTGACTGGAACAACATTGTGTACTCTCTCCCTCTTGTGTTCCACCTCAAG	1140

OY	1141	TCTGACGAATGACACTCCCAATTTTGGAGAACCGAAGAAGAAATTGCGGGTTTCACTCCT	1200
Dd	1141	TCTGACGAATGACACTCCCAATTTTGGAGAACCGAAGAAGAAATTGCGGGTTTCACTCCT	1200
OY	1201	CCGTGCCAGCTGAGACCCTCCAGGCTTCGCGGTGAAGAACTGCCTTGTCGGGTTTTTCG	1260
Dd	1201	CCGTGCCAGCTGAGACCCTCCAGGCTTCGCGGTGAAGAACTGCCTTGTCGGGTTTTTCG	1260
OY	1261	TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTGTGTGCGGGTCTGGACTCC	1320
Dd	1261	TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTGTGTGCGGGTCTGGACTCC	1320
OY	1321	CCTCCCAAAGCTACTCTCCATGGGAAAABAAAACTTCTCATCAAAAGCAAGAGCTACAAGAC	1380
Dd	1321	CCTCCCAAAGCTACTCTCCATGGGAAAABAAAACTTCTCATCAAAAGCAAGAGCTACAAGAC	1380
OY	1381	TCTCAGGACAAAGTGTCAACAAGATGAGACGGAATAAGACCGGTTACATCCGAGAGTGTCA	1440
Dd	1381	TCTCAGGACAAAGTGTCAACAAGATGAGACGGAATAAGACCGGTTACATCCGAGAGTGTCA	1440
OY	1441	GAGGTGAGAGCTGTGCTTAAGTCAGAGAAGAGGTGAGGCTGAAGGCTTGAGACTCAGAGA	1500
Dd	1441	GAGGTGAGAGCTGTGCTTAAGTCAGAGAAGAGGTGAGGCTGAAGGCTTGAGACTCAGAGA	1500
OY	1501	TCCCTCTCTGGAGCGAGACCTTGCTACCTACATCACAGAAATGCACTTAAGCCGAGT	1560
Dd	1501	TCCCTCTCTGGAGCGAGACCTTGCTACCTACATCACAGAAATGCACTTAAGCCGAGT	1560
OY	1561	TTGAGAGCAAGCAGGATGAGAGGTGTCCGAGAGGATGACAAGAGCATGCGACTTCTCAT	1620
Dd	1561	TTGAGAGCAAGCAGGATGAGAGGTGTCCGAGAGGATGACAAGAGCATGCGACTTCTCAT	1620
OY	1621	GATATCAAGAGCAGAGCCGGAGCTCCAAAGAAATCAAGAGCAGAGTACCAAGCTCAA	1680
Dd	1621	GATATCAAGAGCAGAGCCGGAGCTCCAAAGAAATCAAGAGCAGAGTACCAAGCTCAA	1680
OY	1681	GTGGAAGAAATGAGGTTGATGATGAATCAAGTTGGAGAAAGATCTTGCTCAGCAAGAGA	1740
Dd	1681	GTGGAAGAAATGAGGTTGATGATGAATCAAGTTGGAGAAAGATCTTGCTCAGCAAGAGA	1740
OY	1741	CGAGGTATCTCTACGAATCTGAGCTGAGAGAGCTCGGGTGTGCTGTAAGAAATTCAAG	1800
Dd	1741	CGAGGTATCTCTACGAATCTGAGCTGAGAGAGCTCGGGTGTGCTGTAAGAAATTCAAG	1800
OY	1801	CGGAAGCGACAGATGTCAAGCTAATACTGTGGAAGGCTTAAGATCAAGGGAAGCTGAA	1860
Dd	1801	CGGAAGCGACAGATGTCAAGCTAATACTGTGGAAGGCTTAAGATCAAGGGAAGCTGAA	1860
OY	1861	GTGSGAGATATGCGAAACTGAGAGAATCAATGCTGAGCAGCAGCTCAAAATTCAGAG	1920
Dd	1861	GTGSGAGATATGCGAAACTGAGAGAATCAATGCTGAGCAGCAGCTCAAAATTCAGAG	1920
OY	1921	CTCCAAGAAACTGAGAAAGGCTGCAAAAGAGCGAGCCGAGAGGAGCTGAGAAACTG	1980
Dd	1921	CTCCAAGAAACTGAGAAAGGCTGCAAAAGAGCGAGCCGAGAGGAGCTGAGAAACTG	1980
OY	1981	CAGAACCGAAGGATTTCTTCTGAAAGGCTACGAAAAGAGCTGTGTGAAAGCTGAGAAAGC	2040
Dd	1981	CAGAACCGAAGGATTTCTTCTGAAAGGCTACGAAAAGAGCTGTGTGAAAGCTGAGAAAGC	2040
OY	2041	CGCCATTTCTTGAAGAAACAAGTAAAGAGCTAGAGACCAATGAGGCTTAAGAGAAAACAGA	2100
Dd	2041	CGCCATTTCTTGAAGAAACAAGTAAAGAGCTAGAGACCAATGAGGCTTAAGAGAAAACAGA	2100
OY	2101	CTGAAAGATGACATCCGACAAAATTCCTCAACATTCACAGAGATGGCTGATTAATTCCTG	2160
Dd	2101	CTGAAAGATGACATCCGACAAAATTCCTCAACATTCACAGAGATGGCTGATTAATTCCTG	2160
OY	2161	GAGCTCGAAGGAACAATCGGAGAGCCCAAGTCTCAGCCCCAGCACCTAGAGAAGTGCACTG	2220
Dd	2161	GAGCTCGAAGGAACAATCGGAGAGCCCAAGTCTCAGCCCCAGCACCTAGAGAAGTGCACTG	2220
OY	2221	AACAGAAAGACGACATATGAGAGAAAGATTAAAGTGTGCAATCAGATTAAGAAA	2280

2221 AAAAGAAAGAGCAGCTATGAGAGAAAGATTAAAGTTGGTGGCAATCGATTAAGAAA 2280
2281 GACCTGGCTGACAAAGAGACACTGAGAGAACATGATGACAGACACGAGAGAGAGCCCAT 2340
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2341 GAGAAAGGCAAAATTTCTCAGCGAACAAGAGCGATGATCAATGATAGATTCCAGATC 2400
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3001 GATGAGGCTTCTGGCGCCCAACGACGAGATTGTATCAACTGCGAAGTGAAGTGAACCATC 3060
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3061 CGCCCGGAGATCAAGGACGAGAGATGACAGCTTACAGCCAGAGCAAAACGATGAGGCT 3120
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3181 GAGCTGCTAAGAAAAAGAGCGGAGTGGAGGCTTGAAGAGAGCTGCTGGGTGATGAGAAA 3240
3181 GAGCTGCTAAGAAAAAGAGCGGAGTGGAGGCTTGAAGAGAGCTGCTGGGTGATGAGAAA 3240
3241 TCCCAATTTGATGCTGGGTGAGAGCTGACAGAGATGCTGAGACCCGAGAAAACAGAGC 3300
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3301 AGGCGAGAGCGGATCAGCGGATCAGAGTCTGCGCAGGTGATGAGAGCTGCGAGTGAAG 3360

3301 AGGCGAGAGCGGATCAGCGGATCAGAGTCTGCGCAGGTGATGAGAGCTGCGAGTGAAG 3360
3361 GAGCAAGAGCTGAGATTCTCGCTGACAGAGGCTCTCAAGAGACAGAGCTGAAGGCC 3420
3361 GAGCAAGAGCTGAGATTCTCGCTGACAGAGGCTCTCAAGAGACAGAGCTGAAGGCC 3420
3421 GAGAGCTTCTGACAGAGCTCAATGACCTGAGAAAGAGATGATGCTTGAATGAAT 3480
3421 GAGAGCTTCTGACAGAGCTCAATGACCTGAGAAAGAGATGATGCTTGAATGAAT 3480
3481 GCCCGAGCTTACAGAGAGGCTGAGACTGAACGAGGCTCAACAGAGGCTTCTGAA 3540
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3541 GAGCAAGCCAAATTACAGCAGCAGATGACCTGACAGAAAAATCATTCTTCGCTGACT 3600
3541 GAGCAAGCCAAATTACAGCAGCAGATGACCTGACAGAAAAATCATTCTTCGCTGACT 3600
3601 CAGAGCTGCAAGAAAGCTTGAATGGCTGATCTTAAGACAGAAAGAGATGACTTG 3660
3601 CAGAGCTGCAAGAAAGCTTGAATGGCTGATCTTAAGACAGAAAGAGATGACTTG 3660
3661 GAGTATCAGCTGGAAGAAATCATTGAGGCTCTATTCTATGAAAGGTGAATGAAGGC 3720
3661 GAGTATCAGCTGGAAGAAATCATTGAGGCTCTATTCTATGAAAGGTGAATGAAGGC 3720
3721 ACTATTTCTCAACAAACCAAACTCATTTGATTTCTGACAGCCAAATGACCAACTGCT 3780
3721 ACTATTTCTCAACAAACCAAACTCATTTGATTTCTGACAGCCAAATGACCAACTGCT 3780
3781 AAAAAGAAAAAGGGTTATTTATGTCAGAGAAAGAGACCTGCTTTTCCACACAGTT 3840
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3841 CCTCTGAGTACAAATGAGCTGAAGCTGGCTCTGAGAGAAAGAGAGCTGCTGACAG 3900
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4201 AAGTGTCTGTGTGTCTGATTAACGTCACATTTGAGAGCGCAGGCAATGATGCTGAA 4260
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4261 TGTGAGTGAATGTGTCAACCCAGTGTCCACATGCTTGGCAGCCATGCGGCTTGCT 4320
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4381 CTCACAGCAAGAGGCTCAGCAGAGCTTGCACCTTGAAGAGGTGATGAAGGTGCCAGG 4440
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QY 61 GCCAGCCGCGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACTTTATGACTCAA 120
Db 79 GCCAGCCGCGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACTTTATGACTCAA 138
QY 121 CAGCAGATGTCCTCTCTTCCGAGAAAGGATATTAATGAGCCCTCTTGTCTCTTTGAA 180
Db 139 CAGCAGATGTCCTCTCTTCCGAGAAAGGATATTAATGAGCCCTCTTGTCTCTTTGAA 198
QY 181 GAATGCGTCAAGCTGCTTGATGAGATTAAAGACGTGACAACTTTGTCCGGAATAT 240
Db 199 GAATGCGTCAAGCTGCTTGATGAGATTAAAGACGTGACAACTTTGTCCGGAATAT 258
QY 241 TCCGACACCAATAGCTAGTTACAGAGCTCCAGCTTCGGCAAGAAGCTTCGAAATCAGA 300
Db 259 TCCGACACCAATAGCTAGTTACAGAGCTCCAGCTTCGGCAAGAAGCTTCGAAATCAGA 318
QY 301 AGTCTGTAGTGTGTGTCACCTTGTCTGAAGTCAAGTGTGTAAGAGAAAGCAACCGG 360
Db 319 AGTCTGTAGTGTGTGTCACCTTGTCTGAAGTCAAGTGTGTAAGAGAAAGCAACCGG 378
QY 361 GACATCATGCTATGAAGTGAAGAAAGAGAGCTTTATTTGGCCAGAGCAAGTTTCA 420
Db 379 GACATCATGCTATGAAGTGAAGAAAGAGAGCTTTATTTGGCCAGAGCAAGTTTCA 438
QY 421 TTTTGAAGAGAGCGGAAACATATTTATCTGAAGCAAGCCCGTGAATCCCGCAATT 480
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QY 481 CAGTATGCTTTAGAGCAAAAATCACTTTATCTGATGAGAGATATCAAGCTTGAGG 540
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QY 541 GACTGCTGTCACTTTGAATAGATAGAAGACAGTTAGTAAACCTGATACGTTT 600
Db 559 GACTGCTGTCACTTTGAATAGATAGAAGACAGTTAGTAAACCTGATACGTTT 618
QY 601 TACCTAGCTGAGTGAATTTGGCTGTTCAAGCGTTCATCTGATGAGATACGTCATCA 660
Db 619 TACCTAGCTGAGTGAATTTGGCTGTTCAAGCGTTCATCTGATGAGATACGTCATCA 678
QY 661 GACATCAAGCTGAGAAACATCTCGTTGACCGCACAGACCATCAAGCTGTGATTTT 720
Db 679 GACATCAAGCTGAGAAACATCTCGTTGACCGCACAGACCATCAAGCTGTGATTTT 738
QY 721 GGAHTGCGCGGAAAAATGAATTCAAAACAGATGATGATGCCAACTCCGATTGGGACC 780
Db 739 GGAHTGCGCGGAAAAATGAATTCAAAACAGATGATGATGCCAACTCCGATTGGGACC 798
QY 781 CCAAGATTACATGAGCTCTCTGAAGTGTGACTGTGATGAACGGGAGTGAAGAAAGCACTTAC 840
Db 799 CCAAGATTACATGAGCTCTCTGAAGTGTGACTGTGATGAACGGGAGTGAAGAAAGCACTTAC 858
QY 841 GGCCTGGACTGAGACTGAGTGCATGAGGCGGATGTCCTATGAGATGATTTATGGAGGA 900
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QY 1141 TCTGACGATGACACTTCCAAATTTTGAATGAACCAAGAAATTCGTGGGTTTCATCTCT 1200
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Db 1219 CCGTGCAGCTAGGCCCTCAGGCTTCCGGGTGAAGAACTCCGCTTTGTGGGGTTTTCG 1278
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QY 1321 CCTGCAGACTAGCTTCCATGGAAGAACTTCTCATGAAAGCAAGAGCTACAGAGC 1380
Db 1339 CCTGCAGACTAGCTTCCATGGAAGAACTTCTCATGAAAGCAAGAGCTACAGAGC 1398
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QY 1441 GAGTGAAGCTGTGCTTATGTCAGAAAGGTTGAGCTGAAGGCTCTGAGACTCAGAGA 1500
Db 1459 GAGTGAAGCTGTGCTTATGTCAGAAAGGTTGAGCTGAAGGCTCTGAGACTCAGAGA 1518
QY 1501 TCCCTCTGAGACAGGACCTTGTCTTACCTTACATCAAGATGCAATGCTTAAAGCAAGT 1560
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Db 1579 TTGAGCAAGACAGGATGAGAGTGTCCAGAGAGATGACAAAGCACTGACCTTCCAT 1638
QY 1621 GATATCAGAGACAGAGCCGGAAGCTCCAGAAATCAAGAGCAAGAGTCAAGGCTCAA 1680
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QY 1741 CGAGTGAATCTTACGATCTGAGCTGAGAGAGTCTCGGCTTGTGCTGAAGATTCAG 1800
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QY 1801 CGGAAAGCAGCAAGATGTCAGCATAACTGTTGAAGCTTAAAGATCAAGGAAAGCTGAA 1860
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QY 1861 GTGGAAGAAATGAGAACTGGAAGATCAATGCTGAGCAGAGCTCAAAATTCAGAGAG 1920
Db 1879 GTGGAAGAAATGAGAACTGGAAGATCAATGCTGAGCAGAGCTCAAAATTCAGAGAG 1938
QY 1921 CTCAGAGAAATGAGAAAGCTGCAAGAGAGGAGCCGAGAGAGAGCTGAGAAAGCTG 1980
Db 1939 CTCAGAGAAATGAGAAAGCTGCAAGAGAGGCTGCAAGAGAGGAGCTGAGAAAGCTG 1998
QY 1981 CAGAAACGAGAGAGATTTCTTCTGAAGGATCAAGAAAGAAAGCTGTGGAAGCTGAGAAAGC 2040
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QY 2041 CGCCATTCCTGAGAAACAGAGTAAAGAGCTAGAGACCAATGAGAGCTGAGAGAAACAGA 2100
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Db 2119 CTGAAGATGACATCCAGCAAAATCCCAACAGATCCAGCAGATGAGCTGATTAATTCG 2178
QY 2161 GAGCTGAGAGAGAAACATGGGAGGSCCAAGTCTCAGCCCAAGACCTTAAGAGTGCAC 2220
Db 2179 GAGCTGAGAGAGAAACATGGGAGGSCCAAGTCTCAGCCCAAGACCTTAAGAGTGCAC 2238
QY 2221 AAAAGAGAGAGACATATGAGAAAGATTTAAAGTGTGGAATCATGATTAAGAA 2280

Db 2239 AAACAGAAAGAGCAGCTATGAGAAAATTAAGTGTGGCAATCAGATTAAGAAA 2298
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Db 2299 GACCTGGCTGACAAAGAGACATCTGAGAAATATGATGACAGACAGAGAGGCCAT 2358
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Db 2419 AGATCCCTGGACAGAGATTTGTGAACTGTGAAGCCAAATTAATTTGACGCAAAATAGC 2478
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Db 2479 AGTCTTTTACCCAAAGGAACATGAAAGGCCCAAGAAAGATGATTTTCTGAATCTGAGCA 2538
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Qy 2701 CAGCTACAGAGTCAAGCTCTCCCTGCGAGAGCGGAGTCAAGTTGACAGCCCTGCG 2760
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Qy 2821 ACAGCAAGAGCTGAAGAGAGATCCAGGCACTCAGCGCACTAAGATGAATCCAGCC 2880
Db 2839 ACAGCAAGAGCTGAAGAGAGATCCAGGCACTCAGCGCACTAAGATGAATCCAGCC 2898
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Db 2899 AAATTTGATGCTTTTGTAAACAGCTGTATCTATATCAGACCTGAGAGCACTTAAC 2958
Qy 2941 CAGCTGACGAGGACAAACGCTGAACCTCAACCAACAACTTCTAATTTCCAAACAACTC 3000
Db 2959 CAGCTGACGAGGACAAACGCTGAACCTCAACCAACAACTTCTAATTTCCAAACAACTC 3018
Qy 3001 GATGAGGCTTTCTGGCCCAACGACGAGATTGTAACTGCGAGAGTGAAGTGAACCTTC 3060
Db 3019 GATGAGGCTTTCTGGCCCAACGACGAGATTGTAACTGCGAGAGTGAAGTGAACCTTC 3078
Qy 3061 CCGCGGAGAGATCAGGAGAGAGATGCACTTACCAAGCAAGAAACGATGAGGCT 3120
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Qy 3121 CTGAAGACCAAGGACCAATGCTGAGAGAAACAGTGTATGAGTTTGAAGGCCCTTAACGAT 3180
Db 3139 CTGAAGACCAAGGACCAATGCTGAGAGAAACAGTGTATGAGTTTGAAGGCCCTTAACGAT 3198
Qy 3181 GAGCTCTAGAAAAGAGAGCGGAGTGGAGGCTGAGAGAGCTCTCTGGGTGATGAGAA 3240
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Qy 3241 TCCCAATTTGAGTGTGGGTTGAGAGCTGACAGAAATGCTGGAACCCGAGAAACAGAC 3300
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Db 3319 AGGCGAGAGCGGATACAGGAGATCAACGAGTCTCGCAGGTGTGAGCTGCGAGTGAAG 3378
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Qy 3421 GAGAGCTCTGACAAAGCTCAATGACCTGAGAAAGAACATGCTTATGATTAATGAAT 3480
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Qy 3481 GCCCGAAGCTTACAGCAAGAGCTGAGAGCTGAACGAGAGCTCAACAGAGGCTTCTGAA 3540
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Qy 3721 ACTATTTCTCAACAAACCAACTCATGATTTTCTGCAAGCCAAATGAGCAACTGCT 3780
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Db 4399 CTCAGACCAAGAGACCAAGAGCTTGAACCTGGAAGGATGATGAAGGTGCCAGG 4458

QY	4441	AAATACAAACGAGGACACAAAGCGCTGGGACAGGAAAGTCACTTGTCTCGAGAGGATCAAAA	4500
Db	4449	AATAACAAACGAGGACACAAAGCGCTGGGACAGGAAAGTCACTTGTCTCGAGAGGATCAAAA	4518
QY	4501	GTCCCATTTATGACAAATGAAGCCAGAAAGCTGGACAGAGGCCGTGGAAAGAAATTTGAG	4560
Db	4519	GTCCCATTTATGACAAATGAAGCCAGAAAGCTGGACAGAGGCCGTGGAAAGAAATTTGAG	4578
QY	4551	CTGTGACCTTTCCGACGGGGATGTATCTATTCAATGTGCGCTTGGTGTCTTCCGAATCGCA	4620
Db	4579	CTGTGACCTTTCCGACGGGGATGTATCTATTCAATGTGCGCTTGGTGTCTTCCGAATCGCA	4638
QY	4631	AATAAGCAAAAGCGAAAAAGCAGAAAGCTATGTAAATCGCTTGGAAACTCCCTGCTG	4680
Db	4639	AATAAGCAAAAGCGAAAAAGCAGAAAGCTATGTAAATCGCTTGGAAACTCCCTGCTG	4698
QY	4661	AAACTGGAAGGTATGATGACCTGTCTAGACATGAACTGACGCTGACCCTTCAATGATGACAGGTG	4740
Db	4699	AAACTGGAAGGTATGATGACCTGTCTAGACATGAACTGACGCTGACCCTTCAATGATGACAGGTG	4758
QY	4741	GTGTGTGGGGGACCGGAGGAAGGGGTCTAACGCCCTGAATGTCTTGAAGAAATCTCCCTAAC	4800
Db	4759	GTGTGTGGGGGACCGGAGGAAGGGGTCTAACGCCCTGAATGTCTTGAAGAAATCTCCCTAAC	4818
QY	4801	CATGTCCCAAGAAATTGAGACAGTCTTCCAAATTTATATATATCAAGACCTGGAAGAGTA	4860
Db	4819	CATGTCCCAAGAAATTGAGACAGTCTTCCAAATTTATATATCAAGACCTGGAAGAGTA	4878
QY	4861	CTCATGATATGACGAGGAAGAGCGGGCATCTGTGTCTTTGTGACCTGTAGAGAAAGTGAACAG	4920
Db	4879	CTCATGATATGACGAGGAAGAGCGGGCATCTGTGTCTTTGTGACCTGTAGAGAAAGTGAACAG	4938
QY	4921	TCCCTGCGCCAGTCCCACTGCTGCTCCAGGCCGACACTCTACCCAAATTTTGAAGCT	4980
Db	4939	TCCCTGCGCCAGTCCCACTGCTGCTCCAGGCCGACACTCTACCCAAATTTTGAAGCT	4998
QY	4981	GTCAAAGGCTGCACTTGTTTGGGGCAGGCAAGATTGAAACGGGCTCTGATCTGTGCA	5040
Db	4999	GTCAAAGGCTGCACTTGTTTGGGGCAGGCAAGATTGAAACGGGCTCTGATCTGTGCA	5058
QY	5041	GCCATGGCCAGCAAAAGTGCTCATTTCTCGGCTACAAACGAAAACCTCAGCAAAATACGTGATC	5100
Db	5059	GCCATGGCCAGCAAAAGTGCTCATTTCTCGGCTACAAACGAAAACCTCAGCAAAATACGTGATC	5118
QY	5101	CGGAAAGAGATAGAGACCTCAGAGCCCTGACAGCTGTATCCACTTCAACCAATTAAGATAC	5160
Db	5119	CGGAAAGAGATAGAGACCTCAGAGCCCTGACAGCTGTATCCACTTCAACCAATTAAGATAC	5178
QY	5161	CTCATTTGGAACCAATMAATTCTACGAATTCGACATGAAGCAGTACAGCTGTGAGGAATTC	5220
Db	5179	CTCATTTGGAACCAATMAATTCTACGAATTCGACATGAAGCAGTACAGCTGTGAGGAATTC	5238
QY	5221	CTGATATGAAGATGACCAATTCCTTGGCACTGTGCTGTGTGGCGGCTTCCAAACAGCTTC	5280
Db	5239	CTGATATGAAGATGACCAATTCCTTGGCACTGTGCTGTGTGGCGGCTTCCAAACAGCTTC	5298
QY	5281	CTGTGTCTCAATGTCGACAGTGAACAGCGCAAGGGCAGGAGAGAGTACTTGTCTGTGTTTC	5340
Db	5299	CTGTGTCTCAATGTCGACAGTGAACAGCGCAAGGGCAGGAGAGAGTACTTGTCTGTGTTTC	5358
QY	5341	CACGAATTTGAGAGTGTGTGGAATCTTACGGAAGACGTACCCGACAGAGATCTCAAG	5400
Db	5359	CACGAATTTGAGAGTGTGTGGAATCTTACGGAAGACGTACCCGACAGAGATCTCAAG	5418
QY	5401	TGAGATGCTTACCTTTGGCCCTTTGCCCTTACAGAGAACCTTACTGTTTGTGACCACTTC	5460
Db	5419	TGAGATGCTTACCTTTGGCCCTTTGCCCTTACAGAGAACCTTACTGTTTGTGACCACTTC	5478
QY	5461	AACTACTCTGAAGTAAATTGAATCCAGGCAAGCTCTTCAAGCAGGAGCCCTGTGCCGAGCG	5520
Db	5479	AACTACTCTGAAGTAAATTGAATCCAGGCAAGCTCTTCAAGCAGGAGCCCTGTGCCGAGCG	5538

OY		5521	TACCTGGACAATCCCGAACCCGCGCTCCTGGGCGCTGCATTTCCTCAGAGGATTTAC	5580
Dd		5539	TACTGGACATCCCCGAACC CGCCTACCTGGGCGCTGCCATTTCCTCAGAGGATTTAC	5598
OY		5581	TTGGCGTCTCTCAATCACGAGATAAATTAAGGGTCATTGTGTCGAAAGGAAAACCTCGTAGA	5640
Dd		5589	TTGGCGTCTCTCATACAGAGATAAATTAAGGGTCATTGTGTCGAAAGGAAAACCTCGTAGA	5658
OY		5641	GAGTCGCGCATCTGAACCAACCCGCGGCGCTGCACCTCCCGCAGCGACCCCAACAGCGA	5700
Dd		5659	GAGTCGCGCATCTGAACCAACCCGCGGCGCTGCACCTCCCGCAGCGACCCCAACAGCGA	5718
OY		5701	GGCCCAACCCAAGTAAACAGACGATCACCAAGCGGTGGCCCTCCAGCCGAGCGCCGCC	5760
Dd		5719	GGCCCAACCCAAGTAAACAGACGATCACCAAGCGGTGGCCCTCCAGCCGAGCGCCGCC	5778
OY		5761	GAAAGCCCACCAAGCCACCCGCGAGAGCCCAAGACACACCCACCGCTACCCGAGGCGAGACC	5820
Dd		5779	GAAAGCCCACCAAGCCACCCGCGAGAGCCCAAGACACACCCACCGCTACCCGAGGCGAGACC	5838
OY		5821	GAGCTGCGCAGGGCAAAGTCTCTGGCGCGCCCTCTGAGCGAGAGAAGTCCCGCGCGG	5880
Dd		5839	GAGCTGCGCAGGGCAAAGTCTCTGGCGCGCCCTCTGAGCGAGAGAAGTCCCGCGCGG	5898
OY		5881	ATGCTCAGCAGCGGAGAGAGCGGTCGCCCGGAGGCGTGTTGAAGACAGCAGCAGGCG	5940
Dd		5899	ATGCTCAGCAGCGGAGAGAGCGGTCGCCCGGAGGCGTGTTGAAGACAGCAGCAGGCGG	5958
OY		5941	CGGCTGCTCGCGGAGGCGCTGAGAGACCCCGCTGTCCAGGTGAACAGAGGAGCGGAG	6000
Dd		5959	CGGCTGCTCGCGGAGGCGCTGAGAGACCCCGCTGTCCAGGTGAACAGAGGAGCGGAG	6018
OY		6001	AGTGCCTCTCAAGTTTTCACAGGTTTACACCTGTAACCTATTATGACTGGAATTAAGCG	6060
Dd		6019	AGTGCCTCTCAAGTTTTCACAGGTTTACACCTGTAACCTATTATGACTGGAATTAAGCG	6078
OY		6061	GACAACTGCGAGCTAATCTGTCAGACCTTGAAGATCATCAGCTGATGAGAGAAATCCGG	6120
Dd		6079	GACAACTGCGAGCTAATCTGTCAGACCTTGAAGATCATCAGCTGATGAGAGAAATCCGG	6138
OY		6121	CAGCAGGTTGAAAAAGTCTGTCTGAGAACAGATTATTGC	6159
Dd		6139	CAGCAGGTTGAAAAAGTCTGTCTGAGAACAGATTATTATGC	6177
 RESULT 4 US-10-325-430-10 ; Sequence 10, Application US/10325430 ; Publication No. US20030153525A1 ; GENERAL INFORMATION: ; APPLICANT: Millennium Pharmaceuticals, Inc ; APPLICANT: Siles-Santiago, Immaculada ; APPLICANT: Rosenfeld, Julie Beth ; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING ; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207, ; TITLE OF INVENTION: 32838, 336 and 52908 ; FILE REFERENCE: MPI01-294PILNM ; CURRENT APPLICATION NUMBER: US/10/325,430 ; CURRENT FILING DATE: 2002-12-19 ; PRIOR APPLICATION NUMBER: US 60/341,953 ; PRIOR FILING DATE: 2001-12-19 ; NUMBER OF SEQ ID NOS: 21 ; SOFTWARE: FastSeq for Windows Version 4.0 ; SEQ ID NO 10 ; LENGTH: 6574 ; TYPE: DNA ; ORGANISM: Homo Sapiens US-10-325-430-10 Query Match 100.0%; Score 6159; DB 16; Length 6574; Best Local Similarity 100.0%; Fred. No. 0; Matches 6159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				

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Db 2299 GACCTGCTGCAAGAGAGCACTGAGAAATCATGATGAGAGACACGAGGAGAGGCCAT 2358
QY 2341 GAGAGGGGCAAAATTTCTCAGCGAAACAGAGGCCAGATGATCAATGATTCAGATTC 2400
Db 2359 GAGAGGGGCAAAATTTCTCAGCGAAACAGAGGCCAGATGATCAATGATTCAGATTC 2418
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PRIOR APPLICATION NUMBER: US 60/457,901
PRIOR FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: US 60/468,775
PRIOR FILING DATE: 2003-05-08
PRIOR APPLICATION NUMBER: US 60/471,614
PRIOR FILING DATE: 2003-05-19
PRIOR APPLICATION NUMBER: US 60/478,742
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: US 60/488,529
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/491,156
PRIOR FILING DATE: 2003-07-30
PRIOR APPLICATION NUMBER: US 60/499,594
PRIOR FILING DATE: 2003-09-02
PRIOR APPLICATION NUMBER: US 60/506,332
PRIOR FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 136
SOFTWARE: FastSeq for Windows Version 4.0
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LENGTH: 6574
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (19) ... (6180)
US-10-757-262-51

Query Match 100.0%; Score 6159; DB 18; Length 6574;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3721 ACTATTCTCAACAAACCAACCATGATGATTTTCTGCAAGCCCAAAATGAGCCAACTGCT 3780
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|
Db 3739 ACTATTCTCAACAAACCAACCATGATGATTTTCTGCAAGCCCAAAATGAGCCAACTGCT 3798
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|
QY 3781 AAAAGAAAAAGGTTTATTTAGTCGACGAAAGAGACCTGCTTTACCAACAGGTT 3840
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|
Db 3799 AAAAGAAAAAGGTTTATTTAGTCGACGAAAGAGACCTGCTTTACCAACAGGTT 3858
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|
QY 3841 CCTCTCAATTAATAGCTGAAGCTGAGGCTTCTGAGAGAAAGAAAGAGTGGCTGTGAGAG 3900
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|
Db 3859 CCTCTCAATTAATAGCTGAAGCTGAGGCTTCTGAGAGAAAGAAAGAGTGGCTGTGAGAG 3918
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|
QY 3901 CTAGAGAAAGCCTTCAAGAAAGCCGCAATGAGCTCGGCTCGCCCGGAGAGAAAGCTGCC 3960
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Db	3919	CTAGAGAAAGCCCTTCAAGAAAGCCGCATCGAGCTCCGGTCCGCCGGGAGGAAGCTCC	3978
OY	3961	CACCGCAAGCAACGAGCAACCAACCATCAAGCAAGCCACCGGAGAGATC	4020
Db	3979	CACCGCAAGCAACGAGCAACCAACCATCAAGCAAGCCACCGGAGAGATC	4038
OY	4021	GCCATTCGCGCATCGTGGGTGCGCAAGCAACGACCGCATGATGCTGTGGCC	4080
OY	4081	CCGCCATCCAGCCCGCAGAAAGAGCTTCTCACTCCAGAGAAATTAACTGGGCTTAAG	4140
Db	4099	CCGCATTCACGCGGAGAAAGAGCTTCACTCCAGAGAAATTAACTGGGCTTAAG	4158
OY	4141	GAAACGATCACCACAATTTCTCTACCGATTCAAAGTAACTGAACATGCAACCA	4200
Db	4159	GAAACGATCACCACAATTTCTCTACCGATTCAAAGTAACTGAACATGCAACCA	4218
OY	4201	AAGTGTGCTGTGTCTGTGATACCGTGCACCTTTGAGAGCCGACGATCCAAATGTCTGAA	4260
Db	4219	AAGTGTGCTGTGTGTCTGTGATACCGTGCACCTTTGAGAGCCGACGATCCAAATGTCTGAA	4278
OY	4261	TGTCAAGTGAATGTTCACCCCAAGTGTCCACGTCTTGCCAGCACCTGGCGCTTGCT	4320
Db	4279	TGTCAAGTGAATGTTCACCCCAAGTGTCCACGTCTTGCCAGCACCTGGCGCTTGCT	4338
OY	4321	GCTGAATATGCAACACCTTCAACGAGGCTCTGCGCGTGAACAAATGAATCTCCCAAGT	4380
Db	4339	GCTGAATATGCAACACCTTCAACGAGGCTCTGCGCGTGAACAAATGAATCTCCCAAGT	4398
OY	4381	CTCCAGACCAAGAGCCCGACAGCAGCTTGCACCTGAAAGGATGAAAGTCCCAAG	4440
Db	4399	CTCCAGACCAAGAGCCCGACAGCAGCTTGCACCTGAAAGGATGAAAGTCCCAAG	4458
OY	4441	AATAACAACGAGGACAGCAAGGCGTGGGACAGAAATCATTTGCTCTGAGGGATCAAA	4500
Db	4459	AATAACAACGAGGACAGCAAGGCGTGGGACAGAAATCATTTGCTCTGAGGGATCAAA	4518
OY	4501	GTCCTCATTTATGACAAATGAAGCCAGAACTGAGACAGAGCCGGTGGAGAAATTGAG	4560
Db	4519	GTCCTCATTTATGACAAATGAAGCCAGAACTGAGACAGAGCCGGTGGAGAAATTGAG	4578
OY	4561	CTGTGCTTTCCGACGGGAGATGATCTAATTCAATGTGCGTTGTGCTTCCGACTTCGA	4620
Db	4579	CTGTGCTTTCCGACGGGAGATGATCTAATTCAATGTGCGTTGTGCTTCCGACTTCGA	4638
OY	4621	AATAAGCCAAAGCAGAAAGAAAGCAGAAAGCTGATCTAAACGCTGTGAAATCTCCGCTG	4680
Db	4639	AATAAGCCAAAGCAGAAAGAAAGCAGAAAGCTGATCTAAACGCTGTGAAATCTCCGCTG	4698
OY	4681	AAACTGGAAGTGAATGACCGCTTGAACATGAATGCAACGCTGCCCTTCACTGAACAGGTG	4740
Db	4699	AAACTGGAAGTGAATGACCGCTTGAACATGAATGCAACGCTGCCCTTCACTGAACAGGTG	4758
OY	4741	GTTGTTGGTGGCACAACGAGAAAGGCTCTAAGGCCCTGAAATGCTTTGAAATCTCCCTTAAC	4800
Db	4759	GTTGTTGGTGGCACAACGAGAAAGGCTCTAAGGCCCTGAAATGCTTTGAAATCTCCCTTAAC	4818
OY	4801	CATGTCCCAAGAAATTGAGCAGTCTTCCAAATTTATTTATCAAGGACCTGGAGAAAGCTA	4860
Db	4819	CATGTCCCAAGAAATTGAGCAGTCTTCCAAATTTATTTATCAAGGACCTGGAGAAAGCTA	4878
OY	4861	CTCATGATAGCAGGAGAAAGCCGGGCACTGTGCTTGTGACGTGAAAGAAAGTGAACAG	4920
Db	4879	CTCATGATAGCAGGAGAAAGCCGGGCACTGTGCTTGTGACGTGAAAGAAAGTGAACAG	4938
OY	4921	TCCCTGGCCCAAGTCCCACTGCTGCGCCACCGCAACATCTCACCCAAATTTTGAAGCT	4980
Db	4939	TCCCTGGCCCAAGTCCCACTGCTGCGCCACCGCAACATCTCACCCAAATTTTGAAGCT	4998
OY	4981	GTCAGAGGCTGCCACTTGTGTTGGGACAGGCAAGTTGAGAACGGGCTTGTCAATCTGTGCA	5040

Db	4999	GTCAAGGCGTCGCCACTTGTGTTTGGGCGAGCAAGATTGAGACGGGCTCTGCATCTGTGCA	5058
QY	5041	GCCATGCCAGCAAGAGTGTCTATTCGCGTCAACAAGAAACCTCAGCAAAATCTGCATC	5100
Db	5059	GCCATGCCAGCAAGAGTGTCTATTCGCGTCAACAAGAAACCTCAGCAAAATCTGCATC	5118
QY	5101	CGGAAAGAAATGAGACCTCAGAGCCGTGACGCTTATTCATCTTCAACCAATTACGATAC	5166
Db	5119	CGGAAAGAAATGAGACCTCAGAGCCGTGACGCTTATTCATCTTCAACCAATTACGATAC	5178
QY	5161	CTCATTTGAAACCAATMAATTTCTACGAAATCGACATGAAGAGTACACCTCGAGGAATTC	5222
Db	5179	CTCATTTGAAACCAATMAATTTCTACGAAATCGACATGAAGAGTACACCTCGAGGAATTC	5233
QY	5221	CTGGAATGAATGACCATTCCTTGGACCTGCTGTGTGTTTCCGCTCTTCCACAGCTTC	5286
Db	5239	CTGGAATGAATGACCATTCCTTGGACCTGCTGTGTGTTTCCGCTCTTCCACAGCTTC	5298
QY	5281	CCTGATCTCAATGTCGAGGTGAACAGCGCAGGGCAGCGAGAGAGTACTGTGTGATTC	5344
Db	5299	CCTGATCTCAATGTCGAGGTGAACAGCGCAGGGCAGCGAGAGAGTACTGTGTGATTC	5356
QY	5341	CACGAATTTGAGTGTTCGTGATTTCTTACGGAAGACGTAGCCGCAACAGATCTCAAG	5400
Db	5359	CACGAATTTGAGTGTTCGTGATTTCTTACGGAAGACGTAGCCGCAACAGATCTCAAG	5418
QY	5401	TGAGATGCGTTAACCTTTGAGCCCTTTGCGCTACAGAGAACCCTATCTGTTTGTGAACCACTTC	5466
Db	5419	TGAGATGCGTTAACCTTTGAGCCCTTTGCGCTACAGAGAACCCTATCTGTTTGTGAACCACTTC	5478
QY	5461	AACTCACTCGAAGTAATTGAGATCCAGGACAGCTCTTCAGCAGGAGACCCCTGCCAGAGC	5520
Db	5479	AACTCACTCGAAGTAATTGAGATCCAGGACAGCTCTTCAGCAGGAGACCCCTGCCAGAGC	5538
QY	5521	TACCTGGAACATCCCGAACCAGCGGCTACCTGGGCGCTGCAATTTCTCAGAGCGCATTTAC	5580
Db	5539	TACCTGGAACATCCCGAACCAGCGGCTACCTGGGCGCTGCAATTTCTCAGAGCGCATTTAC	5598
QY	5581	TTGGCGTCTCATACACAGATTAATAATTAAGGTCATTTGCTGCAAGGGAAACCTGCTGAG	5640
Db	5599	TTGGCGTCTCATACACAGATTAATAATTAAGGTCATTTGCTGCAAGGGAAACCTGCTGAG	5658
QY	5641	GAGTCGCGGCACTGAACACACACCGGCGCCGCTCACCTCCGCGACAGCCCAACAAGCA	5700
Db	5659	GAGTCGCGGCACTGAACACACACCGGCGCCGCTCACCTCCGCGACAGCCCAACAAGCA	5718
QY	5701	GAGCCCAACCACTGAACACAGACCATCAACAAGGCGGTGCTCAAGCCCAAGCGCGGCC	5760
Db	5719	GAGCCCAACCACTGAACACAGACCATCAACAAGGCGGTGCTCAAGCCCAAGCGCGGCC	5778
QY	5761	GAAAGCCCCAGACACCCGCGAGACCAAGCAACCCCAACCGCTACCGCGAGGGCGGAC	5820
Db	5779	GAAAGCCCCAGACACCCGCGAGACCAAGCAACCCCAACCGCTACCGCGAGGGCGGAC	5838
QY	5821	GAGCTGGCGAGGGGCAAGTCTCTCGAGCGGCCCTCGAGAGGAGAGAGTCCCGCGCGG	5880
Db	5839	GAGCTGGCGAGGGGCAAGTCTCTCGAGCGGCCCTCGAGAGGAGAGAGTCCCGCGCGG	5898
QY	5881	ATGCTCAGCAACGCGAGAGAGCGGTCCCGCGGAGCGTGTGTTGAAGCAACAGCAGGAGC	5940
Db	5899	ATGCTCAGCAACGCGAGAGAGCGGTCCCGCGGAGCGTGTGTTGAAGCAACAGCAGGAGC	5958
QY	5941	CGGTCGCTCTGGGAGCGCTGAGAGACCCGCGTGTCCAGGTGAACAAGGAGAGGGCAG	6000
Db	5959	CGGTCGCTCTGGGAGCGCTGAGAGACCCGCGTGTCCAGGTGAACAAGGAGAGGGCAG	6018
QY	6001	AGTGCCTCTCAAGTTTTCAGGTTTAACTGTCACCTATATATGACCTGGAATTAAGAGT	6060
Db	6019	AGTGCCTCTCAAGTTTTCAGGTTTAACTGTCACCTATATATGACCTGGAATTAAGAGT	6078
QY	6061	GACAACTGCGACGTAACTGTGATCTTAGAGATATCCAGCTGAATGAGAAATCCGG	6120
Db	6079	GACAACTGCGACGTAACTGTGATCTTAGAGATATCCAGCTGAATGAGAAATCCGG	6138

QY	1081	TCGAAATTGACTGGAAACAATCTGTGTAACCTCTCTCCCTCCCTTGTTGCCACCTCAAG	1140
Db	1135	TCGAAATTGACTGGAAACAATCTGTGTAACCTCTCCCTCCCTTGTTGCCACCTCAAG	1194
QY	1141	TCGAGAGATGACACCTCCCAATTTTATATGAAACAAGAAAGAAATCGTGGGTTCAATCCCT	1200
Db	1195	TCGAGAGATGACACCTCCCAATTTTATATGAAACAAGAAAGAAATCGTGGGTTCAATCCCT	1254
QY	1201	CGGTGCACTGAGCCCTCAAGGCTTCTCGGGTGAAGAACTGCGTTTGTGGGGTTTTCG	1260
Db	1255	CGGTGCACTGAGCCCTCAAGGCTTCTCGGGTGAAGAACTGCGTTTGTGGGGTTTTCG	1314
QY	1261	TACAGCAAGGCACTGGGGATTTCTTGGTATGATCTGAGTCTGTTGTGTCGGGCTTGAATCC	1320
Db	1315	TACAGCAAGGCACTGGGGATTTCTTGGTATGATCTGAGTCTGTTGTGTCGGGCTTGAATCC	1374
QY	1321	CCTGCCAAGACTAGCTCCATGTGAAAAAGAACTTCTCATCAAAAGCAAAAGACTCAAGAC	1380
Db	1375	CCTGCCAAGACTAGCTCCATGTGAAAAAGAACTTCTCATCAAAAGCAAAAGACTCAAGAC	1434
QY	1381	TCGACGGACAACTGTCCAAATGTGAGTCAGGAAATGACCCGGTTTCATCCGAGATGTCA	1440
Db	1435	TCGACGGACAACTGTCCAAATGTGAGTCAGGAAATGACCCGGTTTCATCCGAGATGTGTCA	1494
QY	1441	GAGGTGAGGCTGTGCTTATGTCAAGAGAGGTGAGCTGAAAGCCTCTGAGACTCAGAGA	1500
Db	1495	GAGGTGAGGCTGTGCTTATGTCAAGAGAGGTGAGCTGAAAGCCTCTGAGACTCAGAGA	1554
QY	1501	TCCCTCCCTGGAGCAGAGACCTTGCTCTCTCACTCACAGATCAGTACGTTAAACGAAGT	1560
Db	1555	TCCCTCCCTGGAGCAGAGACCTTGCTCACTCACTCAAGATCAGTACGTTAAACGAAGT	1614
QY	1561	TTGGAGCAAGCACGATGAGAGGTGTCCAGAGAGATGACAAAGACCTCGAGCTTCTCAT	1620
Db	1615	TTGGAGCAAGCACGATGAGAGGTGTCCAGAGAGATGACAAAGACCTCGAGCTTCTCAT	1674
QY	1621	GATATCAAGAGCAGAGCCCGGAGCTCCAGAAATCAAAGCAGAGTACCAAGCTCAA	1680
Db	1675	GATATCAAGAGCAGAGCCCGGAGCTCCAGAAATCAAAGCAGAGTACCAAGCTCAA	1734
QY	1681	GTGGAAGAAATGAGGTTGATGATGAAATGATGGAAAGGATCTTGCTCAGCAAGAGA	1740
Db	1735	GTGGAAGAAATGAGGTTGATGATGAAATGATGGAAAGGATCTTGCTCAGCAAGAGA	1794
QY	1741	CGAGATGATCTCTACGAATCTTGAAGTGAAGAGTCTCGGCTTGCTGTAAGATTCAG	1800
Db	1795	CGAGATGATCTCTACGAATCTTGAAGTGAAGAGTCTCGGCTTGCTGTAAGATTCAG	1854
QY	1801	CGAAAGGCGACAGATGTCAAGATTAACGTGTGAAGCTTAAGATCAAGGAAAGCTCGAA	1860
Db	1855	CGAAAGGCGACAGATGTCAAGATTAACGTGTGAAGCTTAAGATCAAGGAAAGCTCGAA	1914
QY	1861	GTGAGAGATATGCGAATCTGAGAGAATCAATGCTGAGACGAGCTCAAAATTCAGAG	1920
Db	1915	GTGAGAGATATGCGAATCTGAGAGAATCAATGCTGAGACGAGCTCAAAATTCAGAG	1974
QY	1921	CTCCAGAGAACTGAGAGGCTG-----	1945
Db	1975	CTCCAGAGAACTGAGAGGCTGTAAGAACGACGACGAGGCTCAAGCTGCTGAG	2034
QY	1946	-----CAAAAGAGCGAGCCGAGAGGAGCTGAGAGAAGCTGCAAGCCGAG	1992
Db	2035	AAATATCCGCCAGGCAAAAGAGCGAGCCGAGAGGAGCTGAGAGAAGCTGCAAGCCGAG	2094
QY	1993	GATTTCTTCTGAAGGCTATCAGAAAGAGCTGAGAGCTGAGGAAAGCGCGCAATTCCTG	2052
Db	2095	GATTTCTTCTGAAGGCTATCAGAAAGAGCTGAGAGCTGAGGAAAGCGCGCAATTCCTG	2154
QY	2053	GAGAAACAAGGTAAAGACTAGAGACATGAGAGGCTGAGAAACAGACTGAAGAGATGAC	2112
Db	2155	GAGAAACAAGGTAAAGACTAGAGACATGAGAGGCTGAGAAACAGACTGAAGAGATGAC	2214
QY	2113	ATCCAGACAAATCCCAAGAGATTCAGCAAGATGGCTGATTAATTCGTGAGCTCGAAG	2172

Db	2215	ATCCAGACAAATTC	CCAA	CAGATCC	AGAGATGG	CTGATTA	AAATTC	CTGAGACT	CGA	AAG	2274
Qy	2173	AAAATCTGGGAG	GGCCCA	AGTCTC	AGCCGAC	CTTA	GAATG	GCATCT	GA	AAAG	2232
Db	2275	AAACATCGGAG	AGCCCA	AGTCTC	AGCCGAC	CTTA	GAATG	GCATCT	GA	AAAG	2234
Qy	2233	CAGCATATAG	AGAAAA	GAATTT	AAAGTGT	TGACAT	CTCAGAT	TAAG	AAAG	AAGACT	2232
Db	2235	CAGCATATAG	AGAAAA	GAATTT	AAATGTT	TGACAT	CTCAGAT	TAAG	AAAG	AAGACT	2234
Qy	2293	AAGGAGCA	CTGGAGA	CA	TGATG	CA	GAGCA	CA	CGAG	AGAGGCCCAT	2352
Db	2395	AAGGAGCA	CTGGAGA	CA	TGATG	CA	GAGCA	CA	CGAG	AGAGGCCCAT	2454
Qy	2353	ATTCTCAG	GAACAG	AAAGCCG	TGATG	CAATCT	CAATG	ATTC	CA	AGTCCCT	2412
Db	2455	ATTCTCAG	GAACAG	AAAGCCG	TGATG	CAATCT	CAATG	ATTC	CA	AGTCCCT	2514
Qy	2413	CAGAGATT	TGGA	CTGTCT	GAAGCC	CAATTA	CTTG	CAGCAAA	TAG	CAGTCTTTT	2472
Db	2515	CAGAGATT	TGGA	CTGTCT	GAAGCC	CAATTA	CTTG	CAGCAAA	TAG	CAGTCTTTT	2574
Qy	2473	CAAGGA	ACATGA	AGGCCCA	AGAGAG	TGATTT	CTGA	CTC	AGGCA	ACAGAA	2532
Db	2575	CAAGGA	ACATGA	AGGCCCA	AGAGAG	TGATTT	CTGA	CTC	AGGCA	ACAGAA	2634
Qy	2533	CTGGAGCA	CAGGCT	GGAGATT	GAGGCC	CGA	AA	CTG	AGAG	CAGACTG	2592
Db	2635	CTGGAGCA	CAGGCT	GGAGATT	GAGGCC	CGA	AA	CTG	AGAG	CAGACTG	2694
Qy	2593	AAGATCAC	CCCA	CAAGCA	CA	AGTGA	CA	AGAA	TGGCTG	CTGGA	2652
Db	2695	AAGATCAC	CCCA	CAAGCA	CA	AGTGA	CA	AGAA	TGGCTG	CTGGA	2754
Qy	2653	CGGAGAGT	CAGTCT	TAGAGCA	CGAGAG	CA	AGAA	CTG	AGGCT	CAAGCC	2712
Db	2755	CGGAGAGT	CAGTCT	TAGAGCA	CGAGAG	CA	AGAA	CTG	AGGCT	CAAGCC	2814
Qy	2713	CTACAGCT	CTCCCT	CGAGAG	CGGAGT	CA	CA	ATTGA	CAGCC	CTG	2772
Db	2815	CTACAGCT	CTCCCT	CGAGAG	CGGAGT	CA	CA	ATTGA	CAGCC	CTG	2874
Qy	2773	GCCCTG	AGAGCC	CAGCTT	CGC	CAGGCG	CA	AGAG	CA	AGGCA	2832
Db	2875	GCCCTG	AGAGCC	CAGCTT	CGC	CAGGCG	CA	AGAG	CA	AGGCA	2934
Qy	2833	GAAGAG	GATCC	CAGGCA	CT	CA	CGGCA	CA	TATG	ATGA	2892
Db	2935	GAAGAG	GATCC	CAGGCA	CT	CA	CGGCA	CA	TATG	ATGA	2994
Qy	2893	CTTCGT	AA	CAGCTG	TATCA	TGATCA	CA	AGCTG	AGAGG	CA	2952
Db	2995	CTTCGT	AA	CAGCTG	TATCA	TGATCA	CA	AGCTG	AGAGG	CA	3054
Qy	2953	GACAA	CGCTGA	CTCA	CA	CA	CAAA	CTT	CTA	CTT	3012
Db	3055	GACAA	CGCTGA	CTCA	CA	CA	CAAA	CTT	CTA	CTT	3114
Qy	3013	GGGCG	CA	ACG	CGA	AGTT	GTAT	CA	AGTGA	AGTGA	3072
Db	3115	GGGCG	CA	ACG	CGA	AGTT	GTAT	CA	AGTGA	AGTGA	3174
Qy	3073	ACGGA	CGAG	GATG	CA	AGCTT	TA	CCAG	CAG	CA	3132
Db	3175	ACGGA	CGAG	GATG	CA	AGCTT	TA	CCAG	CAG	CA	3234
Qy	3133	TGCA	CCAT	GTCT	GA	AGAA	CA	GGTCA	TG	GA	3192
Db	3235	TGCA	CCAT	GTCT	GA	AGAA	CA	GGTCA	TG	GA	3294
Qy	3193	AAAAG	CGAG	AGT	GGAG	GGCT	CTG	AG	AGG	CT	3252

Db 3295 AAAGACGGCAGTGGAGGCGCTGGAGAGCGTCTGGGTGATGAGAATCCAGTTTGAG 3354
Qy 3253 TGTCCGGGTTGAGAGGTGAGAGAAATGCTGGAGACCGAGAAACAGAGCGGGGAGAGCC 3312
Db 3355 TGTCCGGGTTGAGAGGTGAGAGAAATGCTGGAGACCGAGAAACAGAGCGGGGAGAGCC 3414
Qy 3313 GATCAGCGGATCACCGAGTCTCGCCAGGTGTGGAGCTGGCAGTGAAGAGCACAAGGCT 3372
Db 3415 GATCAGCGGATCACCGAGTCTCGCCAGGTGTGGAGCTGGCAGTGAAGAGCACAAGGCT 3474
Qy 3373 GAGATTCTGCTCTGAGAGAGGCTCTCAAGAGCAGAGCTGAAGGCCAGAGCTCTCT 3432
Db 3475 GAGATTCTGCTCTGAGAGAGGCTCTCAAGAGCAGAGCTGAAGGCCAGAGCTCTCT 3534
Qy 3433 GACAGGCTCAATGACCTGGAGAAAGACATGCTTAATGCTTAATGCTTAATGCTTAAT 3492
Db 3535 GACAGGCTCAATGACCTGGAGAAAGACATGCTTAATGCTTAATGCTTAATGCTTAAT 3594
Qy 3493 CAGCAGAGCTGGAGACTGAAAGAGAGCTCAAGAGGCTCTGGAGAGCAGAGCCAA 3552
Db 3595 CAGCAGAGCTGGAGACTGAAAGAGAGCTCAAGAGGCTCTGGAGAGCAGAGCCAA 3654
Qy 3553 TTACAGCAGCAGATGAGACCTGCAAGAAATCAATTTTCGCTGACTCAAGGACTGCA 3612
Db 3655 TTACAGCAGCAGATGAGACCTGCAAGAAATCAATTTTCGCTGACTCAAGGACTGCA 3714
Qy 3613 GAGGCTCTGATGAGGCTGATCTTAAGAGCAGAAAGAGTGAATGAGTGAATGAGTGA 3672
Db 3715 GAGGCTCTGATGAGGCTGATCTTAAGAGCAGAAAGAGTGAATGAGTGAATGAGTGA 3774
Qy 3673 GAAAAATTCAAGTTCTATTCTCATGAAAAAGTGAATGAGAGCACTATTTCGAA 3732
Db 3775 GAAAAATTCAAGTTCTATTCTCATGAAAAAGTGAATGAGAGCACTATTTCGAA 3834
Qy 3733 CAAGCAAACTCATTTGATTTTTCGAAAGCAAAATGAGCAACCTGCTAATAAAGAAAG 3792
Db 3835 CAAGCAAACTCATTTGATTTTTCGAAAGCAAAATGAGCAACCTGCTAATAAAGAAAG 3892
Qy 3793 GGTATTATTAGTCGACGGAAGAGACCTGCTTTACCAACAGGTTCTCTGCAATAC 3852
Db 3893 -----AGGTTCTCTGCAATAC 3909
Qy 3853 AATGAGCTGAAAGCTGCGCTGGAGAGAGAAAGCTCGCTGTGAGAGTGAAGAGCC 3912
Db 3910 AATGAGCTGAAAGCTGCGCTGGAGAGAGAAAGCTCGCTGTGAGAGTGAAGAGCC 3969
Qy 3913 CTTCAAGAGACCCGATCGAGTCCGCTCGCCCGGAGAGAGCTGCCACCGCAAGGA 3972
Db 3970 CTTCAAGAGACCCGATCGAGTCCGCTCGCCCGGAGAGAGCTGCCACCGCAAGGA 4029
Qy 3973 AGGAGACACCCACACCCATTCACGCGCAAGCCAGCGAGAGAGTCCGATGTCGCC 4032
Db 4030 AGGAGACACCCACACCCATTCACGCGCAAGCCAGCGAGAGAGTCCGATGTCGCC 4089
Qy 4033 ATGCTGCGGTGCGCAGAGACCAAGCCAGTGAAGCTGCTGAGCCCGGCAATCAG 4092
Db 4090 ATGCTGCGGTGCGCAGAGACCAAGCCAGTGAAGCTGCTGAGCCCGGCAATCAG 4149
Qy 4093 CGCAGAAAGAGTCTTCAACTCAGAGAAATTAAGTCCGCTTTAAGAGACGATGAC 4152
Db 4150 CGCAGAAAGAGTCTTCAACTCAGAGAAATTAAGTCCGCTTTAAGAGACGATGAC 4209
Qy 4153 CACAAATATTCCTCAACCGATTCAAGTGAAGCTGAACATGCGAGCCCAAGTGTCTG 4212
Db 4210 CACAAATATTCCTCAACCGATTCAAGTGAAGCTGAACATGCGAGCCCAAGTGTCTG 4269
Qy 4213 TGTCTGGATTAACGTTGAGAGCGCAGGAGTCAAAATGCTCAAAATGCTCAAGTGA 4272
Db 4270 TGTCTGGATTAACGTTGAGAGCGCAGGAGTCAAAATGCTCAAAATGCTCAAGTGA 4329
Qy 4273 TGTCAACCCCAAGTCTCAAGTGTGCTGAGAGCCAGCTGCGCTGCTGTAATGAC 4332
Db 4330 TGTCAACCCCAAGTCTCAAGTGTGCTGAGAGCCAGCTGCGCTGCTGTAATGAC 4389

Qy 4333 ACACACTTCAACGAGGCTTCTGCGGTGACAAATGAACTCCCGAGGTCTCCAGACCAAG 4392
Db 4390 ACACACTTCAACGAGGCTTCTGCGGTGACAAATGAACTCCCGAGGTCTCCAGACCAAG 4449
Qy 4393 GAGCCAGCAGAGCTTGGACCTGGAAGGTGATGAAGTCCAGAAATTAACAAACA 4452
Db 4450 GAGCCAGCAGAGCTTGGACCTGGAAGGTGATGAAGTCCAGAAATTAACAAACA 4509
Qy 4453 GGAACGAAAGGCTGGGACAGAAAGTACATTTGCTCTGAGAGGATCAAAATCTCTATTA 4512
Db 4510 GGAACGAAAGGCTGGGACAGAAAGTACATTTGCTCTGAGAGGATCAAAATCTCTATTA 4569
Qy 4513 GACAAATGAAGCAGAGAGAGCTGACAGAGGCGGTGGAAGAAATTTGAGCTGTGCTCC 4572
Db 4570 GACAAATGAAGCAGAGAGAGCTGACAGAGGCGGTGGAAGAAATTTGAGCTGTGCTCC 4629
Qy 4573 GACGGGATGATATTAATCATGATGCGGTGCTCCGAACTGCAAAATACGCCAA 4632
Db 4630 GACGGGATGATATTAATCATGATGCGGTGCTCCGAACTGCAAAATACGCCAA 4689
Qy 4633 GCA----- 4635
Db 4690 GAGAGTGTCCATATACATGAAAGATGAAATCTCACCCGACACCACTGTGCGCGG 4749
Qy 4636 ----- 4635
Db 4750 AGAACCTTACTTGTGCTAGCTCCAGCTTCCCTGACAAACAGCGCTGAGTCAACGCTTA 4809
Qy 4636 -----GAAAAAGCAAGCTGATCTAACTG 4662
Db 4810 GAATCAGTTGTGCGAGGTGAGAGTTTCTAGGAAAAAGCAAGAGCTGATCTAACTG 4869
Qy 4663 CTTGGAATCTCCCTGCTGAACTGGAAGTGAATGACCGTCTGACATGAATGCACTG 4722
Db 4870 CTTGGAATCTCCCTGCTGAACTGGAAGTGAATGACCGTCTGACATGAATGCACTG 4929
Qy 4723 CCCTTCAGTGAACAGGTGCTGTTGGTGGGACACGGAAGAGGCTCAAGCCCTGAAATGTC 4782
Db 4930 CCCTTCAGTGAACAGGTGCTGTTGGTGGGACACGGAAGAGGCTCAAGCCCTGAAATGTC 4989
Qy 4783 TTGAAAACTCCCTTAACCCATGCTCCAGAGATTTGAGCAGTCTTCAAAATTAATTA 4842
Db 4990 TTGAAAACTCCCTTAACCCATGCTCCAGAGATTTGAGCAGTCTTCAAAATTAATTA 5049
Qy 4843 AAGACCTGGAAGAGTACTCATGATGAGAGAGAAAGCGGCACTGTGCTGTGGAC 4902
Db 5050 AAGACCTGGAAGAGTACTCATGATGAGAGAGAAAGCGGCACTGTGCTGTGGAC 5109
Qy 4903 GTGAAGAAAGTGAACAGTCCCTGCGCCAGTCCCACTGCGCCAGCGGCAATCTCA 4962
Db 5110 GTGAAGAAAGTGAACAGTCCCTGCGCCAGTCCCACTGCGCCAGCGGCAATCTCA 5169
Qy 4963 CCAACATTTTGAAGCTGTCAAGGCTGCACTGTTTGGGACAGGCAAGATTGAGAC 5022
Db 5170 CCAACATTTTGAAGCTGTCAAGGCTGCACTGTTTGGGACAGGCAAGATTGAGAC 5229
Qy 5023 GGGCTCTGATCTGTGACAGCAATGCCAGCAAGTGTGATTTCTCGCTTACACGAAAC 5082
Db 5230 GGGCTCTGATCTGTGACAGCAATGCCAGCAAGTGTGATTTCTCGCTTACACGAAAC 5289
Qy 5083 CTCAGAAATATGTCATCCGGAAGAGATGAGACCTCGAGACCTCGAGCTGTATCCAC 5142
Db 5290 CTCAGAAATATGTCATCCGGAAGAGATGAGACCTCGAGACCTCGAGCTGTATCCAC 5349
Qy 5143 TTCACCAATTAAGTATCTCATTTGGAACCAATTAATTTACGAATGACATGAGCAG 5202
Db 5350 TTCACCAATTAAGTATCTCATTTGGAACCAATTAATTTACGAATGACATGAGCAG 5409
Qy 5203 TACAGCTCGAGGAATCTCTGATGAAGATGACATCTTGGACCTGCTGTGTTGCC 5262
Db 5410 TACAGCTCGAGGAATCTCTGATGAAGATGACATCTTGGACCTGCTGTGTTGCC 5469

QY	5263	GCCTCTCCAAAGCTCCCTGCTCAATCGAGGTAAACAAGCGCAGGCGAGGAG	5322
Db	5470	GCCCTTTCCAAAGCTCCCTGCTCAATCGAGGTAAACAAGCGCAGGCGAGGAG	5529
QY	5323	GAGTACTGCTGTGTTCCACGAATTTGGAGTTCGTGGAATTCCTAACGGAAGACGTAC	5382
Db	5530	GAGTACTGCTGTGTTCCACGAATTTGGAGTTCGTGGAATTCCTAACGGAAGACGTAC	5589
QY	5383	CGCAACAGACGATCTCAAGTGGAGTGGCTTAACTTTGGCTTTGGCTTACAGAGAACCTTAT	5442
Db	5590	CGCAACAGACGATCTCAAGTGGAGTGGCTTAACTTTGGCTTTGGCTTACAGAGAACCTTAT	5649
QY	5443	CTGTTTGGAGCCCACTTCAACTCACTCGAAGTAAATTGAATCCAGGCAAGCTTCAGAGA	5502
Db	5650	CTGTTTGGAGCCCACTTCAACTCACTCGAAGTAAATTGAATCCAGGCAAGCTTCAGAGA	5709
QY	5503	GGGACCCCTGCGCCGAGCGTACCTGGACATCCCGAAACCCGCGTACCTGGAGCCCTGCATT	5562
Db	5710	GGGACCCCTGCGCCGAGCGTACCTGGACATCCCGAAACCCGCGTACCTGGAGCCCTGCATT	5769
QY	5563	TCCTCAGAGAGCATTTTACTTGGCGTCTCATACCAAGATTAATTAAAGGTCAATTGCTGC	5622
Db	5770	TCCTCAGAGAGCATTTTACTTGGCGTCTCATACCAAGATTAATTAAAGGTCAATTGCTGC	5829
QY	5623	AAGGAAACCTGTGAAGAGTCCGCACTGAACACCAACCGGCGCCCGTCCACTTCCTCCGC	5682
Db	5830	AAGGAAACCTGTGTAAAGAGTCCGCACTGAACACCAACCGGCGCCCGTCCACTTCCTCCGC	5889
QY	5683	AGCAGCCCCCAACAACGAGAGGCCACCAACGTAACAACGAGACATCAACAAGCGCGTGGCC	5742
Db	5890	AGCAGCCCCCAACAACGAGAGGCCACCAACGTAACAACGAGACATCAACAAGCGCGTGGCC	5949
QY	5743	TCACGCCCAAGCGCGCCCGAAGGCCCCAGCCACCCGCGAGACCAAGCACACCCACCGC	5802
Db	5950	TCACGCCCAAGCGCGCCCGAAGGCCCCAGCCACCCGCGAGACCAAGCACACCCACCGC	6009
QY	5803	TACCCGAGAGGGCGGACCGAGCTGCGCAGAGGACAAGTCTCTGGCGCGCCCTTGGAGGCA	5862
Db	6010	TACCCGAGAGGGCGGACCGAGCTGCGCAGAGGACAAGTCTCTGGCGCGCCCTTGGAGGCA	6069
QY	5863	GAGAACTCCCCGCGCGGATGCTCAGACAGCGGAGAGAGCGGTCCTCCGGAGAGGCTGTT	5922
Db	6070	GAGAACTCCCCGCGCGGATGCTCAGACAGCGGAGAGAGCGGTCCTCCGGAGAGGCTGTT	6129
QY	5923	GAGAAGCAGCAGCAGGAGCGCGCTGCTGCGGAGCGCTGAGAGACCCGCTGTCCAGAGTG	5982
Db	6130	GAGAAGCAGCAGCAGGAGCGCGCTGCTGCGGAGCGCTGAGAGACCCGCTGTGTCCAGAGTG	6189
QY	5983	AACAAGGGAAGAGGGCAGAGTGCCTCTCAAGTTTCAACGTTTAACTGTCACTATAT	6042
Db	6190	AACAAGGCTGTGGAGCAGTCTTCAAGTATTAATCTAGCCAGAAAAACCAATCTCATCT	6249

Query Match	91.9%	Score 5661.4	DB 13	Length 6165
Best Local Similarity	95.8%	Pred. No. 0		
Matches 5944	Conservative 0	Mismatches 16	Indels 243	Gaps 3
QY 1	ATGTTGAAGTTCAAAATATGAGGCGGGAATCCTTTGATGTCGTGGCTGTCGAACCCATT	60		
DB 1	ATGTTGAAGTTCAAAATATGAGGCGGGAATCCTTTGATGTCGTGGCTGTCGAACCCATT	60		
OY 61	GCCAGCCGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACTTTATGACTAA	120		
DB 61	GCCAGCCGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACTTTATGACTAA	120		
OY 121	CAGCAGATGTCCTCTTCTTCCGGAAGGATATTAGATGCCCTCTTGTCTCTTGAA	180		
DB 121	CAGCAGATGTCCTCTTCTTCCGGAAGGATATTAGATGCCCTCTTGTCTCTTGAA	180		
OY 181	GAATGCATCAGCTGCTCTGATATGAATTTAAGCACTGACCACTTTGTCCGAAGAT	240		
DB 181	GAATGCATCAGCTGCTCTGATATGAATTTAAGCACTGACCACTTTGTCCGAAGAT	240		
OY 241	TCCGACACCTATAGCTAGTTACAGAGCTCCAGCTTGGGAAAAGCACTTGAAGTCA	300		
DB 241	TCCGACACCAATAGCTAGTTACAGAGCTCCAGCTTGGGAAAAGCACTTGAAGTCA	300		
OY 301	AGCTCTTGAGTTGTGCTCACTTGTCTGAAGTGCAGGTGATTAAGAGAAAGCAACGGG	360		
DB 301	AGCTCTTGAGTTGTGCTCACTTGTCTGAAGTGCAGGTGATTAAGAGAAAGCAACGGG	360		
OY 361	GACATCTATGCTATGAAAGTATGAAGAAGGCTTTATTTGGCCGAGACAGTTTCA	420		
DB 361	GACATCTATGCTATGAAAGTATGAAGAAGGCTTTATTTGGCCGAGACAGTTTCA	420		
OY 421	TTTTTGAAGAAAGCGGACATATTTATCTGAAGACCAAGCCGTGATCCCCCAATTA	480		
DB 421	TTTTTGAAGAAAGCGGACATATTTATCTGAAGACCAAGCCGTGATCCCCCAATTA	480		
OY 481	CAGTATGCTTTCAAGACAAAATACCTTTATCTGATGAGAAATATCAGCTTGAGGG	540		
DB 481	CAGTATGCTTTCAAGACAAAATACCTTTATCTGATGAGAAATATCAGCTTGAGGG	540		
OY 541	GACTTGCTGTCACTTTGAATAGATATAGAGACCACTTAAATCTGATACAGTTT	600		
DB 541	GACTTGCTGTCACTTTGAATAGATATAGAGACCACTTAAATCTGATACAGTTT	600		
OY 601	TACCTAGCTGAGTATTTGGCGTTCACAGCCTTCACTGAATGAGGATACGTGATCGA	660		
DB 601	TACCTAGCTGAGTATTTGGCGTTCACAGCCTTCACTGAATGAGGATACGTGATCGA	660		
OY 661	GACATCAAGCCTGAGAACATTTCTGTGACCGGACAGGACACATCAAGCTGTGATTTT	720		
DB 661	GACATCAAGCCTGAGAACATTTCTGTGACCGGACAGGACACATCAAGCTGTGATTTT	720		
OY 721	GGATTCGCGGAAAATGAATTTCAAAACAGATGCTGAATGCCAATCTCCATTTGGACC	780		
DB 721	GGATTCGCGGAAAATGAATTTCAAAACAGATGCTGAATGCCAATCTCCATTTGGACC	780		
OY 781	CCAGATTAACATGAGCTCCGGAAGTCTGATCTGATGAAACGGGGATGGAAGGACCTAC	840		
DB 781	CCAGATTAACATGAGCTCCGGAAGTCTGATCTGATGAAACGGGGATGGAAGGACCTAC	840		
OY 841	GGCCTGACCTGTGACTGGTGTCACTGGGCGCTGATTCCTATGAGATTTATGGAGA	900		
DB 841	GGCCTGACCTGTGACTGGTGTCACTGGGCGCTGATTCCTATGAGATTTATGGAGA	900		
OY 901	TCCCTCTTGGGAGGAACTCTGCGAAGACCTTCAATTAACATTTATGAATTTCAACGG	960		
DB 901	TCCCTCTTGGGAGGAACTCTGCGAAGACCTTCAATTAACATTTATGAATTTCAACGG	960		
OY 961	TTTTTGAATTTCAAGATGACCCCAAAAGTACAGTACTTTCTTGATCTGATTTCAAGC	1020		
DB 961	TTTTTGAATTTCAAGATGACCCCAAAAGTACAGTACTTTCTTGATCTGATTTCAAGC	1020		

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1981 AATATCCGCAAGCAAG 2040
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Qy 4636 -----GAAAGCAGAGCTGATGCTAACTG 4662
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RESULT 8
US-10-791-666-1
; Sequence 1, Application US/10791666
; Publication No. US20040209297A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Fiddle, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/791,666
; PRIOR FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335

PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6165
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-791-666-1
Query Match 91.9%; Score 5661.4; DB 18; Length 6165;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 5944; Conservative 0; Mismatches 16; Indels 243; Gaps 3;
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OY	5743	TCCAAGCCAGCGCGCGCCGGAAGGCCCAAGCCACCCGCGAGAGCAACACCCCAACCGC	5802
Db	5896	TCCAAGCCAGCGCGCGCCGGAAGGCCCAAGCCACCCGCGAGAGCAACACCCCAACCGC	5955
OY	5803	TACCGGAGGGGGCGGACCGAGCTGGGACAGGGACCAAGTCCCTGGGCGCGCCCTTGGAGCGA	5866
Db	5956	TACCGGAGGGGGCGGACCGAGCTGGGACAGGGACCAAGTCCCTGGGCGCGCCCTTGGAGCGA	6018
OY	5863	GAGAAAGTCCCGCGCGCGATGCTCAGACAACGCGAGAGAGAGCGGTCCCGCGAGAGCGTGT	5922
Db	6016	GAGAAAGTCCCGCGCGCGATGCTCAGACAACGCGAGAGAGAGCGGTCCCGCGAGAGCGTGT	6075
OY	5923	GAAAGCAGCAGCAGGAGGCGGCTGCTCGGAGACCCGCTGTCTCCAGGTG	5988
Db	6076	GAAAGCAGCAGCAGGAGGCGGCTGCTCGGAGACCCGCTGTCTCCAGGTG	6135
OY	5983	AACAAAGGAAAGAGGCGAGAGTGC	6005
Db	6136	AACAAAGTCTGGGACCAAGTCTTC	6158

	Query March	91.8%	Score 5651.8	DB 18	Length 8656	
Db	Best Local Similarity	95.5%	Pred. No. 0			
	Matches 5960	Conservative	0	Mismatches 37	Indels 246	Gaps 4
QY	1	ATGTTGAAGTTC	CAATAATGAGCCGGAAATCCTTTGATGCTGTGCTGTAACCCATT	60		
Db	51	ATGTTGAAGTTC	CAATAATGAGCCGGAAATCCTTTGATGCTGTGCTGTAACCCATT	110		
QY	61	GCCAGCCGGGCTT	CCAGGCTGAATCTGTCTTCCAGGGGAAACCACTTATAGCTCA	120		
Db	111	GCCAGCCGGGCTT	CCAGGCTGAATCTGTCTTCCAGGGGAAACCACTTATAGCTCA	170		
QY	121	CAGAGATGTCTC	CTTTCCCGAAGGATATTAGATGCCCTTTTGTCTCTTTGAA	180		
Db	171	CAGAGATGTCTC	CTTTCCCGAAGGATATTAGATGCCCTTTTGTCTCTTTGAA	230		
QY	181	GAATGCACTACG	CTCTCTGTATGAAATTAAAGCCGAGACCACTTGTCCGAA---G	237		
Db	231	GAATGCACTACG	CTCTCTGTATGAAATTAAAGCCGAGACCACTTGTCCGAAAGTG	290		
QY	238	TATTCGCAACAT	AGCTGAGTTACAGAGCTCCAGCTTGGGCAAGACTTTCGAACTC	297		
Db	291	TATTCGCAACAT	AGCTGAGTTACAGAGCTCCAGCTTGGGCAAGACTTTCGAAAGTC	350		
QY	298	AGAGTCTTGTAG	TTGTGTCTCACTTTGCTGAAGTGCAGGTGTAAAGAGAAAGCAAC	357		
Db	351	AGAGTCTTGTAG	TTGTGTGTCTCACTTTGCTGAAGTGCAGGTGTAAAGAGAAAGCAAC	410		
QY	358	GGGACATCTAT	GTGCTATGAAAGTGTGAAGAAAGGCTTATATGGCCAGAGAGAGGT	417		
Db	411	GGGACATCTAT	GTGCTATGAAAGTGTGAAGAAAGGCTTATATGGCCAGAGAGAGGT	470		
QY	418	TCATTTTGTGA	GAAGACGGAAACATATTATCTCGAAGCACAGCCGCTGATCCCCCA	477		
Db	471	TCATTTTGTGA	GAAGACGGAAACATATTATCTCGAAGCACAGCCGCTGATCCCCCA	530		
QY	478	TTACAGTATGCT	TTTCAGGACAAAATCACTTTATCTGATGAGAAATATAGCTGGA	537		
Db	531	TTACAGTATGCT	TTTCAGGACAAAATCACTTTATCTGATGAGAAATATAGCTGGA	590		
QY	538	GGGACTTGCTG	CACTTTTGAATGATATGAGACCACTTAGATGAAAACTGTATACG	597		
Db	591	GGGACTTGCTG	CACTTTTGAATGATATGAGACCACTTAGATGAAAACTGTATACG	650		
QY	598	TTTATCTAGCT	AGCTGATTTTGGCTGTTCACAGCGTTTCATCTGATGGGATAGCTGAT	657		
Db	651	TTTATCTAGCT	AGCTGATTTTGGCTGTTCACAGCGTTTCATCTGATGGGATAGCTGAT	710		
QY	658	CGAGCATCAAG	CCGAGAACATTCCTGTTGACCGCACAGGACATCAAGCTGTGAT	717		
Db	711	CGAGCATCAAG	CCGAGAACATTCCTGTTGACCGCACAGGACATCAAGCTGTGAT	770		
QY	718	TTTGATCTGCG	CGCAAAATGATTTCAACAAGATGTAATGCCAACTCCGATTGGG	777		
Db	771	TTTGATCTGCG	CGCAAAATGATTTCAACAAGATGTAATGCCAACTCCGATTGGG	830		
QY	778	ACCCAGATTA	ATAGGCTCTGAATGCTGACTGTGAAGAACGGGAGTGGAAAAAGCAC	837		
Db	831	ACCCAGATTA	ATAGGCTCTGAATGCTGACTGTGAAGAACGGGAGTGGAAAAAGCAC	890		

[illegible]

QY	1918	GAGCTCCAAAGAAACTGGAGAGGCT-----	1944
Db	1971	GAGCTCCAAAGAAACTGGAGAAAGCTGTAAAGCCAGCACGAGGCCACCGAGCTGCTG	2030
QY	1945	-----GCMAAGGAGCGAGCCGAGAGGGAGCTGGAGAACTGCGAACCGA	1989
Db	2031	CAGAAATATCCGCCAGGCAAAAGAGCCGAGAGGGAGCTGGAGAACTGCGAACCGA	2090
QY	1990	GAGGATTTCTTCTGAAAGCATCAGAAAGAGCTGTGAGACTGAGAAACGCCCGCATTTCT	2049
Db	2091	GAGGATTTCTTCTGAAAGCATCAGAAAGAGCTGTGAGACTGAGAAACGCCCGCATTTCT	2150
QY	2050	CTGGAGAAACAAGGTAAAGAGACTAGAGCAATGAGAGCTGTAGAGAAACAATCTGAAGAT	2109
Db	2151	CTGGAGAAACAAGGTAAAGAGACTAGAGCAATGAGAGCTGTAGAGAAACAATCTGAAGAT	2210
QY	2110	GACATCCAGCAAAATCCCAACAGATCAGAGATGAGCTGATAAATTTCTGGAGCTGAA	2169
Db	2211	GACATCCAGCAAAATCCCAACAGATCAGAGATGAGCTGATAAATTTCTGGAGCTGAA	2270
QY	2170	GAGAAACATCGGAGAGGCCCAAGTCTCAGCCAGCACCTAGAAAGTGCACCTGAACAGAAA	2229
Db	2271	GAGAAACATCGGAGAGGCCCAAGTCTCAGCCAGCACCTAGAAAGTGCACCTGAACAGAAA	2330
QY	2230	GAGCAGCACTATGAGAGAAAGATTAATAGTTGGACATCAGATATAAAGAAAGACTGGCT	2289
Db	2331	GAGCAGCACTATGAGAGAAAGATTAATAGTTGGACATCAGATATAAAGAAAGACTGGCT	2390
QY	2290	GACAAAGAGACACTGGAGAACTGATCAGACACAGAGAGAGAGGCCCATGGAAGAGGC	2349
Db	2391	GACAAAGAGACACTGGAGAACTGATCAGAGACAGAGAGAGAGGCCCATGGAAGAGGC	2450
QY	2350	AAAATTTCTCAGACGAAACAGAAAGCCAGATCATGCTATGATTTCCAAGATCAGATCCCTG	2409
Db	2451	AAAATTTCTCAGACGAAACAGAAAGCCAGATCATGCTATGATTTCCAAGATCAGATCCCTG	2510
QY	2410	GAAACAGAGATTTGTGGAACTGTCTGAAAGCCATTAACCTTGACAGAAATAGCAGTCTTTT	2469
Db	2511	GAAACAGAGATTTGTGGAACTGTCTGAAAGCCATTAACCTTGACAGAAATAGCAGTCTTTT	2570
QY	2470	ACCCAAAGGAACATGAAGAGGCCCAAGAGAGATGATTTCTGAACCTCAGGCAACGAAATTT	2529
Db	2571	ACCCAAAGGAACATGAAGAGGCCCAAGAGAGATGATTTCTGAACCTCAGGCAACGAAATTT	2630
QY	2530	TACCTGGAGACACAGGCTGGGAAGTTGGAAGCCAGAAACGGAACCTGGAGAGCAGCTG	2589
Db	2631	TACCTGGAGACACAGGCTGGGAAGTTGGAAGCCAGAAACGGAACCTGGAGAGCAGCTG	2690
QY	2590	GAGAAAGATCAGCCACCAAGACCAACAGTGAACAGATTCGAGCTGGAATCTGGAGACAA	2649
Db	2691	GAGAAAGATCAGCCACCAAGACCAACAGTGAACAGATTCGAGCTGGAATCTGGAGACAA	2750
QY	2650	TTGCGGGAGAGTCACTTAAGACACGAGAGACAGAACTGAGACTCAAGGCCCAGCTCA	2709
Db	2751	TTGCGGGAGAGTCACTTAAGACACGAGAGACAGAACTGAGACTCAAGGCCCAGCTCA	2810
QY	2710	GAGCTACAGCTCTCCCTGCAAGAGCCGGAGTCAACAGTTGACAGCCCTGCAAGCTCA	2769
Db	2811	GAGCTACAGCTCTCTCCCTGCAAGAGCCGGAGTCAACAGTTGACAGCCCTGCAAGCTCA	2870
QY	2770	GCGGCCCTTGAAGAGCCAGCTTTCGCAAGCCGACAGAGCAGAGCTGGAAGAGACACAGCA	2829
Db	2871	GCGGCCCTTGAAGAGCCAGCTTTCGCAAGCCGACAGAGCAGAGCTGGAAGAGACACAGCA	2930
QY	2830	GCTGAAGAGAGATCCAGGCACTCAAGCCCATTAAGATGAATTCAGAGCCAAATTTGAT	2889
Db	2931	GCTGAAGAGAGATCCAGGCACTCAAGCCCATTAAGATGAATTCAGAGCCAAATTTGAT	2990
QY	2890	GCTCTTGCTGAACAGCTGTATCTGTAAATACAGACCTTGAAGAGAGAGCTTAAACAGCTG	2949
Db	2991	GCTCTTGCTGAACAGCTGTATCTGTAAATACAGACCTTGAAGAGAGAGCTTAAACAGCTG	3050
QY	2950	GAGACAAACGCTGAACCTCAACACAAACCTTCTTGTCTCAACCAACTGATGAGGCT	3009

Db 3051 GAGGACACGCTGAACCTCAACACAAAACCTTACTCTTCCAAACACTCGATAGGCT 3110
Qy 3010 TCTGGCCCCAACGACGAGATTGTCAACTGCGAAAGTGAACCATCTCCGCGGAG 3069
Db 3111 TCTGGCCCCAACGACGAGATTGTCAACTGCGAAAGTGAACCATCTCCGCGGAG 3170
Qy 3070 ATCAGGACGAGAGATGACAGCTTACAGGACGAAAGAAAGATGAGGCTCTGAAGACC 3129
Db 3171 ATCAGGACGAGAGATGACAGCTTACAGGACGAAAGAAAGATGAGGCTCTGAAGACC 3230
Qy 3130 ACCGTGCACATGCTGAGGAAACAGTCAATGATTTGAGGCCCTAAACGATGAGCTCTA 3189
Db 3231 ACCGTGCACATGCTGAGGAAACAGTCAATGATTTGAGGCCCTAAACGATGAGCTCTA 3290
Qy 3190 GAAAAAGAGGAGGAGTGGAGGCTGAGAGAGCGCTCTGGGTATGAGAAATCCAGTTT 3249
Db 3291 GAAAAAGAGGAGGAGTGGAGGCTGAGAGAGCGCTCTGGGTATGAGAAATCCAGTTT 3350
Qy 3250 GAGTGTGCGGTTGAGAGCTGACAGAGATGCTGGAACCGAGAAACAGAGCAGGCGGAGA 3309
Db 3351 GAGTGTGCGGTTGAGAGCTGACAGAGATGCTGGAACCGAGAAACAGAGCAGGCGGAGA 3410
Qy 3310 GCCGATCAGGAGATCACCCAGTCTGCCAGGTGTGAGCTGCAAGTGAAGACCAAG 3369
Db 3411 GCCGATCAGGAGATCACCCAGTCTGCCAGGTGTGAGCTGCAAGTGAAGACCAAG 3470
Qy 3370 GCTGAGATTCTGCTGACGAGGCTCAAGAGACAGAGCTGAAGGCCAGAGCTTC 3429
Db 3471 GCTGAGATTCTGCTGACGAGGCTCTCAAGAGACAGAGCTGAAGGCCAGAGCTTC 3530
Qy 3430 TCTGACAGCTCAATGACCTGAGAGAAAGCATGCTTGAATGAATGCCCAAGC 3489
Db 3531 TCTGACAGCTCAATGACCTGAGAGAAAGCATGCTTGAATGAATGCCCAAGC 3590
Qy 3490 TTATACAGAGAGCTGAGAGCTGAAGAGCTCAACAGAGCTTCTGAAAGCAAGCC 3549
Db 3591 TTATACAGAGAGCTGAGAGCTGAAGAGCTCAACAGAGCTTCTGAAAGCAAGCC 3650
Qy 3550 AAATTACAGCAGATGAGACCTGACAGAAATCAATTTCCGCTGACTCAAGAGACTG 3609
Db 3651 AAATTACAGCAGATGAGACCTGACAGAAATCAATTTCCGCTGACTCAAGAGACTG 3710
Qy 3610 CAAAGAGCTCTAGATCGGCTGATCTACTGAAGACAGAAAGATGAGCTTGAAGTATCAG 3669
Db 3711 CAAAGAGCTCTAGATCGGCTGATCTACTGAAGACAGAAAGATGAGCTTGAAGTATCAG 3770
Qy 3670 CTGAAAAACATTCAGGTTCTCTATCTCATGAAAAAGTGAAGAAAGGCACTATTTCT 3729
Db 3771 CTGAAAAACATTCAGGTTCTCTATCTCATGAAAAAGTGAAGAAAGGCACTATTTCT 3830
Qy 3730 CAAACAACCAATCTATTGATTTTCTGCAAGCCAAATGACCAACTGCTTAAAAAGAA 3789
Db 3831 CAAACAACCAATCTATTGATTTTCTGCAAGCCAAATGACCAACTGCTTAAAAAGAA 3890
Qy 3790 AAGGGTTTATTAGTCGACGAGAAAGAACCTGCTTAAACCAACAGGTTCTCTGAG 3849
Db 3891 A-----AGGTTCTCTGAG 3905
Qy 3850 TACATGAGCTGAAGCTGACCTGAGAAAGAGAAAGCTGCTGTCAGACTGAGAA 3909
Db 3906 TACATGAGCTGAAGCTGACCTGAGAAAGAGAAAGCTGCTGTCAGACTGAGAA 3965
Qy 3910 GCCCTTCAAGAAACCGCATGAGCTCCGCTCCGCGAGAGAAAGCTGCCACCGCAA 3969
Db 3966 GCCCTTCAAGAAACCGCATGAGCTCCGCTCCGCGAGAGAAAGCTGCCACCGCAA 4025
Qy 3970 GCAACGAGCCACCAACCACTCAACGCGACACCGGAGGCGACAGATGCCATGCTCC 4029
Db 4026 GCAACGAGCCACCAACCACTCAACGCGACACCGGAGGCGACAGATGCCATGCTCC 4085
Qy 4030 GCATCGTGGGTGCGCAGAGACCAAGCCAGTGCATAGGCTGCTGGGCCGCCATCC 4089

Db 4086 GCCATCGCGGTCCGACAGACCAAGCCAGTGCATGAGCTGTGCCCCCATTC 4145
Qy 4090 AGCCGAGAAAGAGATCTTCAACTCCAGAGAAATTTAGTCGGCGCTTAAAGGAAGCATG 4149
Db 4146 AGCCGAGAAAGAGATCTTCAACTCCAGAGAAATTTAGTCGGCGCTTAAAGGAAGCATG 4205
Qy 4150 CACCAATATTCTCAACCGATTCAAGTGAAGCTGAACATGCAAGCAAAAGTGTCT 4209
Db 4206 CACCAATATTCTCAACCGATTCAAGTGAAGCTGAACATGCAAGCAAAAGTGTCT 4265
Qy 4210 GTGTGTCGGAATACCGTGACCTTTGAGGCGAGGATCCAAATGCTGGAATGTCAGTGTG 4269
Db 4266 GTGTGTCGGAATACCGTGACCTTTGAGGCGAGGATCCAAATGCTGGAATGTCAGTGTG 4325
Qy 4270 ATGTGTCAACCCCAAGTGTCCACGCTTGTGCAAGCACTGCGGCTTCTGTAATAT 4329
Db 4326 ATGTGTCAACCCCAAGTGTCCACGCTTGTGCAAGCACTGCGGCTTCTGTAATAT 4385
Qy 4330 GCCACACACTTCAACGAGGCTTCTGCGGTGAACAAATGAATCCCAAGTCTCAAGC 4389
Db 4386 GCCACACACTTCAACGAGGCTTCTGCGGTGAACAAATGAATCCCAAGTCTCAAGC 4445
Qy 4390 AAGAGCCCAAGAGCTTGCACCTGGAAGGAGTGAAGGTGCCAAGGAATTAACAA 4449
Db 4446 AAGAGCCCAAGAGCTTGCACCTGGAAGGAGTGAAGGTGCCAAGGAATTAACAA 4505
Qy 4450 CGAGGACGCAAGGCTGGAACGAGAGTACATTTCTGTGAGGAGTCAAAAGTCTCATTT 4509
Db 4506 CGAGGACGCAAGGCTGGAACGAGAGTACATTTCTGTGAGGAGTCAAAAGTCTCATTT 4565
Qy 4510 TATGACATGAGAGCCAGAGAAAGCTGACAGAGGCGGTGGAAGAAATTTGAGCTGTGCTT 4569
Db 4566 TATGACATGAGAGCCAGAGAAAGCTGACAGAGGCGGTGGAAGAAATTTGAGCTGTGCTT 4625
Qy 4570 CCCGACGGGAGTGTATCTATTCAATGTGCGGTGTGCTTCCGAATCCGAAATTAACAGCC 4629
Db 4626 CCCGACGGGAGTGTATCTATTCAATGTGCGGTGTGCTTCCGAATCCGAAATTAACAGCC 4685
Qy 4630 AAAGCA----- 4635
Db 4686 AAAGCAATGTCCCATACATACGAAAGATGAATTCACCCGACACACCTGTGCGCC 4745
Qy 4636 ----- 4635
Db 4746 GGGAGAACCTCTTACTTGTGTAAGTCCAGCTTCCCTGACAAACAGCGGTGACCGCC 4805
Qy 4636 -----GAAAAACAGAGCTGATGCTTAA 4659
Db 4806 TTGAATCAGTTGTGCGAGGTGGAGAGTTTCTAGGGAATAACAGAGCTGATGCTTAA 4865
Qy 4660 CTGCTTGAAGAACTCCCGCTGGAACCTGGAAGGTGATGACCGTCTAAGCATGAATCGCAGC 4719
Db 4866 CTGCTTGAAGAACTCCCGCTGGAACCTGGAAGGTGATGACCGTCTAAGCATGAATCGCAGC 4925
Qy 4720 CTGCGCTTCAGTGACAGAGTGTGTGTGAGGACCGAGAGAGGCTTAAACCGCTGAAT 4779
Db 4926 CTGCGCTTCAGTGACAGAGTGTGTGTGAGGACCGAGAGAGGCTTAAACCGCTGAAT 4985
Qy 4780 GTCTTGAATACTCCCTTAAACCATGTCCAGAGAAATGAGCACTTCCAAATTTATAT 4839
Db 4986 GTCTTGAATACTCCCTTAAACCATGTCCAGAGAAATGAGCACTTCCAAATTTATAT 5045
Qy 4840 ATCAAGGACCTGGAAGCTACATCATGATGAAGAGAGACCGGCACTGTGTCTTGTG 4899
Db 5046 ATCAAGGACCTGGAAGCTACATCATGATGAAGAGAGACCGGCACTGTGTCTTGTG 5105
Qy 4900 GACGTGAAGAAAGTGAACAGTCCCTGAGCCAGTCCCACTGCTGCGACCGCAATC 4959
Db 5106 GACGTGAAGAAAGTGAACAGTCCCTGAGCCAGTCCCACTGCTGCGACCGCAATC 5165
Qy 4960 TCACCCCAATTTTGAAGCTGTCAAGGCTGTCACTTGTGAGGAGCAAGCAAGATTGAG 5019
Db 5166 TCACCCCAATTTTGAAGCTGTCAAGGCTGTCACTTGTGAGGAGCAAGCAAGATTGAG 5225

QY 5020 AACGGGCTGATCTGTGAGCATGCCAGCAAGTGTGATCTCCGCTACACGAA 5079
 DB 5226 AACGGGCTGATCTGTGAGCATGCCAGCAAGTGTGATCTCCGCTACACGAA 5285
 QY 5080 AACCTCAGCAAACTGATCGCGAAAGATAGAGACTCAGAGCCCTGACGCTGTATC 5139
 DB 5286 AAGCTCAGCAAACTGATCGCGAAAGATAGAGACTCAGAGCCCTGACGCTGTATC 5345
 QY 5140 CACTTCAACAATTAAGTATCTGATTTGGAACCAATTAATTTACGAATTCAGATGAAG 5199
 DB 5346 CACTTCAACAATTAAGTATCTGATTTGGAACCAATTAATTTACGAATTCAGATGAAG 5405
 QY 5200 CAGTACAGCTCGAGGAATTCCTGATTAAGATGATTCCTTGGACCTGTGTGTTT 5259
 DB 5406 CAGTACAGCTCGAGGAATTCCTGATTAAGATGATTCCTTGGACCTGTGTGTTT 5465
 QY 5260 GCGGCTCTTCCACAGCTTCCCTGTCTCAATCTGTCAGGTGACAGCGCAGGACGCA 5319
 DB 5466 GCGGCTCTTCCACAGCTTCCCTGTCTCAATCTGTCAGGTGACAGCGCAGGACGCA 5525
 QY 5320 GAGGATCTTGTGTGTTTCCAGATTTGAGTGTGTGATTTCTTACGGAAGACT 5379
 DB 5526 GAGGATCTTGTGTGTTTCCAGATTTGAGTGTGTGATTTCTTACGGAAGACT 5585
 QY 5380 AAGCGCAGAGATCTCAAGTGAAGTCCCTTACCTTGGCCCTTACAGAGAACCC 5439
 DB 5586 AAGCGCAGAGATCTCAAGTGAAGTCCCTTACCTTGGCCCTTACAGAGAACCC 5645
 QY 5440 TATCTGTTGTGATCCATCTCACTCACTGAAGTGAATGATTCAGGACGCTCTCA 5499
 DB 5646 TATCTGTTGTGATCCATCTCACTCACTGAAGTGAATGATTCAGGACGCTCTCA 5705
 QY 5500 GAGGAGACCTTCCGCGGAGCTGATCTGACATCTCCGAACTCCGCGCTACTGCGCCCTGCGC 5559
 DB 5706 GAGGAGACCTTCCGCGGAGCTGATCTGACATCTCCGAACTCCGCGCTACTGCGCCCTGCGC 5765
 QY 5560 ATTCTCTGAGAGCATTTACTTGGGTCTCATACCAAGATTAATTAAGGTCATTTGCG 5619
 DB 5766 ATTCTCTGAGAGCATTTACTTGGGTCTCATACCAAGATTAATTAAGGTCATTTGCG 5825
 QY 5620 TGCAGAGGAACTCGTGAAGATCCGACACTGAACACACCGGCGCCCTGCTCACTCC 5679
 DB 5826 TGCAGAGGAACTCGTGAAGATCCGACACTGAACACACCGGCGCCCTGCTCACTCC 5885
 QY 5680 CGAGAGACCTCCCAAGAGAGCCCACTCACTGATCAACAGACATCAACCAAGCGCTG 5739
 DB 5886 CGAGAGACCTCCCAAGAGAGCCCACTCACTGATCAACAGACATCAACCAAGCGCTG 5945
 QY 5740 GCTTCAGGCGGCGCGCGCGGAGGCGGCGGAGGCGGCGGAGGCGGAGGCGGCGG 5799
 DB 5946 GCTTCAGGCGGCGCGCGCGGAGGCGGCGGAGGCGGCGGAGGCGGAGGCGGCGG 6005
 QY 5800 CGCTACCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 5859
 DB 6006 CGCTACCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 6065
 QY 5860 CGAGAGAGTCCCCCGGCGGAGTCTCAGACGCGGAGAGAGCGGTCCCCCGGAGGCTG 5919
 DB 6066 CGAGAGAGTCCCCCGGCGGAGTCTCAGACGCGGAGAGAGCGGTCCCCCGGAGGCTG 6125
 QY 5920 TTTGAAGACAGAGAGGCGGCGGCGGAGGCGGCGGAGGCGGCGGAGGCGGCGG 5979
 DB 6126 TTTGAAGACAGAGAGGCGGCGGCGGAGGCGGCGGAGGCGGCGGAGGCGGCGG 6185
 QY 5980 GTGAACAAGGAGAGGCGGAGGCGGCGGCGGAGGCGGCGGAGGCGGCGGAGGCGG 6039
 DB 6186 GTGAACAAGGAGAGGCGGAGGCGGCGGCGGAGGCGGCGGAGGCGGCGGAGGCGG 6245
 QY 6040 TAT 6042
 DB 6246 TCT 6248

RESULT 10
 US-09-964-956-10
 ; Sequence 10, Application US/09964956
 ; Publication No. US20040043926A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gerlach, Valerie L
 ; APPLICANT: MacDougall, John R
 ; APPLICANT: Smithson, Glenda
 ; APPLICANT: Miller, Isabelle
 ; APPLICANT: Stone, David
 ; APPLICANT: Gunther, Erik
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Grosse, William M
 ; APPLICANT: Alsobrook II, John P
 ; APPLICANT: Lepley, Denise M
 ; APPLICANT: Burgess, Catherine E
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Spyrek, Kimberly A
 ; APPLICANT: Leach, Martin D
 ; APPLICANT: Shinkets, Richard A
 ; TITLE OF INVENTION: No. US20040043926A1e1 Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-124
 ; CURRENT APPLICATION NUMBER: US/09/964,956
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: 60/235,631
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 ; PRIOR APPLICATION NUMBER: 60/235,808
 ; PRIOR FILING DATE: 2000-09-27
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 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/236,065
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/236,066
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/236,135
 ; PRIOR FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: 60/237,434
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/238,321
 ; PRIOR FILING DATE: 2000-10-05
 ; PRIOR APPLICATION NUMBER: 60/238,399
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,396
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/276,667
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/294,823
 ; PRIOR FILING DATE: 2001-05-31
 ; PRIOR APPLICATION NUMBER: 60/304,868
 ; PRIOR FILING DATE: 2001-07-12
 ; NUMBER OF SEQ ID NOS: 127
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 10
 ; LENGTH: 6189
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-964-956-10
 Query Match 91.4%; Score 5631; DB 11; Length 6189;
 Best Local Similarity 95.3%; Pred. No. 0;
 Matches 5944; Conservative 0; Mismatches 45; Indels 246; Gaps 4;
 QY 1 ATGTGAAGTCAATATGAGAGCGGGAATCTTTGATGCTGCGTGAACCACTT 60
 DB 1 ATGTGAAGTCAATATGAGAGCGGGAATCTTTGATGCTGCGTGAACCACTT 60
 QY 61 GCCACCGGCGCTCCAGGCTGAATCTTCTTCCAGGGAACCACTTTATGACTGA 120
 DB 61 GCCACCGGCGCTCCAGGCTGAATCTTCTTCCAGGGAACCACTTTATGACTGA 120

QY 121 CAGCAGATGTCCTCTCTTCCCGAGAGGATATTAGATGCTCTTGTCTTTGAA 180
DB 121 CAGCAGATGTCCTCTCTTCCCGAGAGGATATTAGATGCTCTTGTCTTTGAA 180
QY 181 GAATGACGATGAGCTGCTGTGATGATTAAGCAGTGAACAATTGTCCGGAATAT 240
DB 181 GAATGACGATGAGCTGCTGTGATGATTAAGCAGTGAACAATTGTCCGGAATAT 240
QY 241 TCCGACACCAATAGCTGATTACAGAGCTCCAGCTTGGCAAGGACTTGAAGTACA 300
DB 241 TCCGACACCAATAGCTGATTACAGAGCTCCAGCTTGGCAAGGACTTGAAGTACA 300
QY 301 AGCTTTAGAGTTGGGTCACTTGTGAGTCAAGTGTGTAAGAGAAAGCAACCGG 360
DB 301 AGCTTTAGAGTTGGGTCACTTGTGAGTCAAGTGTGTAAGAGAAAGCAACCGG 360
QY 361 GACATCTATGCTATGAAAGTGAAGAGAGGCTTATTTGGCCAGAGACAGTTTCA 420
DB 361 GACATCTATGCTATGAAAGTGAAGAGAGGCTTATTTGGCCAGAGACAGTTTCA 420
QY 421 TTTTGGAGGAAGGCGGAAATATTATCTGAAAGCAAGCCGTGATCCCAATTA 480
DB 421 TTTTGGAGGAAGGCGGAAATATTATCTGAAAGCAAGCCGTGATCCCAATTA 480
QY 481 CAGATATGCTTTGAGGACAAATAATCACTTTATCTGATGAGGAAATGAGCCTGAGG 540
DB 481 CAGATATGCTTTGAGGACAAATAATCACTTTATCTGATGAGGAAATGAGCCTGAGG 540
QY 541 GACTTCTGTCACTTTTGAATGATATGAGACCAAGTATGATGAAACCTGATACAGTT 600
DB 541 GACTTCTGTCACTTTTGAATGATATGAGACCAAGTATGATGAAACCTGATACAGTT 600
QY 601 TACCTAGCTGAGTATTTGGCTGTTCAAGGCTCATCTGATGGGAAACGTGCATGCA 660
DB 601 TACCTAGCTGAGTATTTGGCTGTTCAAGGCTCATCTGATGGGAAACGTGCATGCA 660
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DB 661 GACATGAGCTTGAAGAACTTCGTGTCGTCGACGCAAGACACATCAAGCTGTGATTTT 720
QY 721 GGATCGCGCGGAAATGAATCAACAGATGATGATGCAAACTCCCGATTGGAGC 780
DB 721 GGATCGCGCGGAAATGAATCAACAGATGATGATGCAAACTCCCGATTGGAGC 780
QY 781 CCAGATTCATGAGCTCTGAAAGTGTGACTGTGATGAACGAGGATGAAAGGACCTAC 840
DB 781 CCAGATTCATGAGCTCTGAAAGTGTGACTGTGATGAACGAGGATGAAAGGACCTAC 840
QY 841 GGCCTGGACTGTGACTGTGCTCACTGTGAGCTGATGCTATGAGATGATTTATGAGGA 900
DB 841 GGCCTGGACTGTGACTGTGCTCACTGTGAGCTGATGCTATGAGATGATTTATGAGGA 900
QY 901 TCCCCCTTCGACGAGGAACTCTGCCGAGAACCTTCAATTAATTTATGAAATTTTCAAGG 960
DB 901 TCCCCCTTCGACGAGGAACTCTGCCGAGAACCTTCAATTAATTTATGAAATTTTCAAGG 960
QY 961 TTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTCTTCTTGAATCTGAATCAAGC 1020
DB 961 TTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTCTTCTTGAATCTGAATCAAGC 1020
QY 1021 TTGTTGTGCGGCGAAGAAAGAGAGTGAAGTGAAGTCTTGTCTGCAATCTTCTTC 1080
DB 1021 TTGTTGTGCGGCGAAGAAAGAGAGTGAAGTGAAGTCTTGTCTGCAATCTTCTTC 1080
QY 1081 TCTAAATTTGACTGGAACAATTCGTAATCTCTCCCTCCCTCGTTCCCACTCAAG 1140
DB 1081 TCTAAATTTGACTGGAACAATTCGTAATCTCTCCCTCCCTCGTTCCCACTCAAG 1140
QY 1141 TCTGACGATGACCTTCAATTTTGAATGACCAAGAAAGAAATTTGTGGGTTTCACTCT 1200
DB 1141 TCTGACGATGACCTTCAATTTTGAATGACCAAGAAAGAAATTTGTGGGTTTCACTCT 1200
QY 1197 TCTGACGATGACCTTCAATTTTGAATGACCAAGAAAGAAATTTGTGGGTTTCACTCT 1197

QY 1201 CCGTGCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGGGGTTTTCG 1260
DB 1198 CCGTGCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGGGGTTTTCG 1257
QY 1261 TACAGGAGGCACTGGGATTTCTTGATGATCTGAGTCTTGTGTGGGTCTGACCTC 1320
DB 1258 TACAGGAGGCACTGGGATTTCTTGATGATCTGAGTCTTGTGTGGGTCTGACCTC 1317
QY 1321 CCTGCAGAGCTAGCTCCATGGAAGAAAGAACTTCTCATCAAGAAAGAGCTAACAGC 1380
DB 1318 CCTGCAGAGCTAGCTCCATGGAAGAAAGAACTTCTCATCAAGAAAGAGCTAACAGC 1377
QY 1381 TCTCAGGACAACTGTACAAAGATGAGAGCAAGAAATGACCCGTTTACATCGAGAGTCA 1440
DB 1378 TCTCAGGACAACTGTCAAAAGATGAGAGCAAGAAATGACCCGTTTACATCGAGAGTCA 1437
QY 1441 GAGGTGAGGCTGTGCTTATGCTACAAAGAGAGTGAAGCTGAAGGCTCTGAGACTCAGAGA 1500
DB 1438 GAGGTGAGGCTGTGCTTATGCTACAAAGAGAGTGAAGGCTCTGAGACTCAGAGA 1497
QY 1501 TCCCTCTGAGACGAGACCTTGTCTACTACATCAAGAAATGCAAGTCTTAAAGCAAGT 1560
DB 1498 TCCCTCTGAGACGAGACCTTGTCTACTACATCAAGAAATGCAAGTCTTAAAGCAAGT 1557
QY 1561 TTGAGGACGACCGGATGAGGTGTCCAGAGAGATGACAAAGCACTGACCTTCTCAT 1620
DB 1558 TTGAGGACGACCGGATGAGGTGTCCAGAGAGATGACAAAGCACTGACCTTCTCAT 1617
QY 1621 GATATCAGAGACGAGCCGAGACCTCCAGAAATCAAGAGCGAGAGTCAACAGCTCA 1680
DB 1618 GATATCAGAGACGAGCCGAGACCTCCAGAAATCAAGAGCGAGAGTCAACAGCTCA 1677
QY 1681 GTGAGAAATGAGCTTATGATGATGAATCAGTTGGAAGAGATCTTGTCTCAGCAAGAGA 1740
DB 1678 GTGAGAAATGAGCTTATGATGATGAATCAGTTGGAAGAGATCTTGTCTCAGCAAGAGA 1737
QY 1741 CGGAGTATCTCTAGCAATCTGAGCTGAGAGAGTCTGCGCTTGTGCTGAAGAAATTAAG 1800
DB 1738 CGGAGTATCTCTAGCAATCTGAGCTGAGAGAGTCTGCGCTTGTGCTGAAGAAATTAAG 1797
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DB 1798 CGGAAAGCAGAGATGCTAGCAATTAATCTTTGAAGCTTAAGATCAAGGAAAGCTGAA 1857
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DB 1858 GTGGAGAAATATGCGAAACTGAGAGAGATCAATGCTGAGCAGCAGCTCAAAATTCAGAG 1917
QY 1921 CTCCAAGAGAACTGAGAGAGCTG----- 1945
DB 1918 CTCCAAGAGAACTGAGAGAGCTGTAAGAAAGCAGACGAGAGCCACCGAGCTGTGACAG 1977
QY 1946 -----CAAGAGCAGAGCCGAGAGGAGCTGAGAGAGCTGAGAGAGCTGAGAGAG 1992
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QY 1993 GATTCTTCTGAAGAGCTACAGAAAGAGAGCTGTGTGAAGCTGAGAGAGCGCGCAATTTCTTG 2052
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QY 2113 ATCCAGACAAATCCCAAGATCCAGAGATGAGTGAATTAATTTCTGAGCTCGAAGAG 2172
DB 2158 ATCCAGACAAATCCCAAGATCCAGAGATGAGTGAATTAATTTCTGAGCTCGAAGAG 2217
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DB 2218 AAACATCGGAGAGCCCAAGTCTCAGCCGAGCCTTAAGAGTCACTGAAGAAAGAG 2277
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Db 2338 AAGGAGACACTGAGAAACATGATGCAAGACACAGAGAGAGAGCCCATGAGAAAGGCATA 2397
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Db 2518 CAAAGGAACATGAAAGGCCCAAGAGAGATGATTTCTGAACTCAGCAACAGAAATTTTAC 2577
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Db 2578 CTGAGACACAGGCTGGGAAAGTTGAGAGGCCAGAAACCGAAACTGAGAGAGACGCTGGAG 2637
Qy 2593 AAGATCAGGCCACCAAGACCAAGTACAGTACAGAAATCGGCTGCTGGAACCTGAGACAAAGATTG 2652
Db 2638 AAGATCAGGCCACCAAGACCAAGTACAGTACAGAAATCGGCTGCTGGAACCTGAGACAAAGATTG 2697
Qy 2653 CGGAGAGTCACTAGAGACAGAGAGAGAACTGAGACTCAGAGCCAGCTCACAGAG 2712
Db 2698 CGGAGAGTCACTAGAGACAGAGAGAGAACTGAGACTCAGAGCCAGCTCACAGAG 2757
Qy 2713 CTGACGCTCTCCCTGAGAGAGGCGGAGTCAAGTTGACAGCCCTGAGAGCTGACGAGGCG 2772
Db 2758 CTGACGCTCTCCCTGAGAGAGGCGGAGTCAAGTTGACAGCCCTGAGAGCTGACGAGGCG 2817
Qy 2773 GCCCTGAGAGACAGCTTTCGAGGCGGAGAGACAGAGCTGGAAGAGACACAGAGAGAGT 2832
Db 2818 GCCCTGAGAGACAGCTTTCGAGGCGGAGAGACAGAGCTGGAAGAGACACAGAGAGAGT 2877
Qy 2833 GAAAGAGAGATCAGGCACTCAGGCACTAGAGATGAATTCAGGCGCAATTTGATGCT 2892
Db 2878 GAAAGAGAGATCAGGCACTCAGGCACTAGAGATGAATTCAGGCGCAATTTGATGCT 2937
Qy 2893 CTTTCTGAACAGCTGTAATCTGTAATCAGAGACCTGAGAGAGACGTTAAACAGAGTACCGAG 2952
Db 2938 CTTTCTGAACAGCTGTAATCTGTAATCAGAGACCTGAGAGAGACGTTAAACAGAGTACCGAG 2997
Qy 2953 GACAAAGCTGAACCTCAACCAAACTTCTACTTGTCCAAACAACTCGATGAGGCTTCT 3012
Db 2998 GACAAAGCTGAACCTCAACCAAACTTCTACTTGTCCAAACAACTCGATGAGGCTTCT 3057
Qy 3013 GCGCGCAACGAGAGATGTAACAATGCGAAGTGAAGTGAACCATCTCCGCGCGAGATC 3072
Db 3058 GCGCGCAACGAGAGATGTAACAATGCGAAGTGAAGTGAACCATCTCCGCGCGAGATC 3117
Qy 3073 ACGGAACGAGAGTGAAGTCTTACAGACCGAAGCAACGATGAGGCTCTGAAGACCAAG 3132
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Qy 3133 TGCACCATGCTGAGAGACAGGTCATGATTTGAGAGGCTTAAACGATGAGCTGTAGAA 3192
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Qy 3253 TGTCCGGTTTGAAGAGTCTGAGAGAAATGCTGAGACACCGAAGAAACAGAGCGAGGAGAGCC 3312
Db 3298 TGTCCGGTTTGAAGAGTCTGAGAGAGATGCTGAGACACCGAAGAAACAGAGCGAGGAGAGCC 3357
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Db 3478 GACAGCTCAATGACCTGAGAGAGAGATGCTATGCTTGAATGAAATGCCCCGAAGCTTA 3537
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Db 3538 CAGCAAGCTGGAGACTGAACGAGAGCTCAAAACAGAGCTTCTGAGAGAGCAAGCCAAA 3597
Qy 3553 TTACAGCAGAGATGAGACCTGAGAGAAATGCAATTTCCGCTGACCTCAAGAGCTGAA 3612
Db 3598 TTACAGCAGCAGATGAGACCTGAGAGAAATGCAATTTCCGCTGACCTCAAGAGCTGAA 3657
Qy 3613 GAAGCTTAGATCGGGCTGATCTTACAGAGACAGAAAGAGTGAAGTGAAGTATCAGCTG 3672
Db 3658 GAAGCTTAGATCGGGCTGATCTTACAGAGACAGAAAGAGTGAAGTGAAGTATCAGCTG 3717
Qy 3673 GAAAAATTGAGGTTCTTATTTCTATGAAAGTGAAGATGAAGAGCACTATTTCTCAA 3732
Db 3718 GAAAAATTGAGGTTCTTATTTCTATGAAAGTGAAGATGAAGAGCACTATTTCTCAA 3777
Qy 3733 CAAACCAATCTATGATTTTCTGCAAGCCAAATGAGCAACCTGCTTAAAGAAAG 3792
Db 3778 CAAACCAATCTATGATTTTCTGCAAGCCAAATGAGCAACCTGCTTAAAGAAAG -- 3835
Qy 3793 GGTATTATTAGTCAGCAGGAAAGAGACCTGCTTACCACACAGAGTTCTCTGAGTAC 3852
Db 3836 -----AGTGCTCTGCAAGTAC 3852
Qy 3853 AATGAGCTGAGAGCTGAGCCCTGAGAGAGAGAAAGTCTGCTGTCAGAGCTGAAGAGCT 3912
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Db 3973 ACGGACCAACCAACCAATGCAAGCAGGCAAGGAGAGAGAGAGAGAGAGAGAGAGAG 4032
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Db 4213 TGTCTGATATCCGTGACCTTTGAGAGCGCAGGAGTCCAAATGTCAGATGTCAGGTGATG 4272
Qy 4273 TGTCAACCCCAATGCTCCAGCTGCTTCCAGGCACTGCGGCTTCCGCTGCTGCTGCTG 4332
Db 4273 TGTCAACCCCAATGCTCCAGCTGCTTCCAGGCACTGCGGCTTCCGCTGCTGCTGCTG 4332
Qy 4333 ACACACTTACCGAGAGCTTCTGCGGTGCAAAATGAACTCCCAAGTCTCCAGAGCAAG 4392
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Db 4393 GAGCCAGCAGAGCTTGAACCTGAGAGAGGTGATGAAGGTGATGAAGGTGATGAAGGTG 4452

QY 4453 GGACAGCAAGGCTGGGACAGAAATGATCTTGTCTTGGAGGATCAAAAGTCCATTTAT 4512
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Db 4453 GGACAGCAAGGCTGGGACAGAAATGATCTTGTCTTGGAGGATCAAAAGTCCATTTAT 4512
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Db 4513 GCAATGAAACCAAGAGAGCTGGACAGAGCCGGTGAAGAAATTTAGCTGTGCCCTTCC 4572
QY 4573 GACGGGAGATGATATTAATGATGTCCGTGGTGGTCTTCCGAATCAAGCCAA 4632
| | | | |
Db 4573 GACGGGAGATGATATTAATGATGTCCGTGGTGGTCTTCCGAATCAAGCCAA 4632
QY 4633 GCA----- 4635
| | | | |
Db 4633 GCAAGATGTCCATACATCTGAAAGATGAAATCTCACCCGACACCACTGTGGCCGGG 4692
| | | | |
QY 4636 ----- 4635
| | | | |
Db 4693 AGAACCCTCTACTGTCTAGCTCCAGCTTCCCTGACAAACAGCGCTGGTCAACCGCTTA 4752
| | | | |
QY 4636 ----- 4662
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Db 4873 CCGTTGATGACCAAGGTGTGTGTGTGGGACCCGAGAAAGGCTCTACGCTCTGAATGTC 4932
| | | | |
QY 4783 TTGAAAACTGCTTAACCCATGTCACAGAAATTTGAGCGATCTTCAAAATTAATTAATC 4842
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Db 4933 TTGAAAACTGCTTAACCCATGTCACAGAAATTTGAGCGATCTTCAAAATTAATTAATC 4992
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QY 4843 AAGACCTGGAGAGACTACTCATGATAGCAGAGAAAGCGGCACTGTCTTGTGAC 4902
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Db 4993 AAGACCTGGAGAGACTACTCATGATAGCAGAGAAAGCGGCACTGTCTTGTGAC 5052
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Db 5113 CCCAATTTTGAAGCTGTCAAGGGCTGCCACTGTTGGGGGAGGCAAGTTAGAAC 5172
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Db 5173 GGGCTCTGATCTGTGACGCCATGCCCAGCAAAATGCTCATTTCCGCTAACAGAAAAC 5232
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| | | | |
Db 5233 CTCAGCAAAATCTGATCTCGGAAAGATAGAGCCTCAGAGCCTGCACTGTATCCAC 5292
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Db 5293 TTCACCAATTAAGATCTCTGTAAGCAATAATTTCTAGAAATGACATGAAGAG 5352
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Db 5353 TACAGGCTCGAAGAAATTCCTGATTAAGATGACATTCCTTGGCACTGTGTGTTCC 5412
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QY 5323 GAGTACTGTGTGTTCACAGAAATTTGAGAGTTCGAGAGTTCTTAAGAAAGACTAGC 5382
| | | | |
Db 5473 GAGTACTGTGTGTTCACAGAAATTTGAGAGTTCGAGAGTTCTTAAGAAAGACTAGC 5532
| | | | |

QY 5383 GGCACAGAGATCTCAAGTGAAGTGTGCTTACTTTTGGCTTTGCTTACAGAGAACCTTAT 5442
| | | | |
Db 5533 GGCACAGAGATCTCAAGTGAAGTGTGCTTACTTTTGGCTTTGCTTACAGAGAACCTTAT 5592
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QY 5443 CTGTTGTGACCCACTTCAACTCACTGAAATTAATTAAGATTCAGGCAAGCTCTCAGCA 5502
| | | | |
Db 5593 CTGTTGTGACCCACTTCAACTCACTGAAATTAATTAAGATTCAGGCAAGCTCTCAGCA 5552
| | | | |
QY 5503 GGGACCCCTGCCCCGAGCTTACTGGAACATCCCGAAACCCGCGTACTTGGGCGCTGCCATT 5562
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Db 5633 GGGACCCCTGCCCCGAGCTTACTGGAACATCCCGAAACCCGCGTACTTGGGCGCTGCCATT 5712
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| | | | |
Db 5713 TCCTCAGAGAGCATTTACTTGGCGTCTCATTAACAGATTAATTAAGGTCATTTGCTGC 5772
| | | | |
QY 5623 AAAGGAAACCTGTGAAGAGTCCGCGCATGAACCAACCGGAGCCGCTCCACTCCGC 5682
| | | | |
Db 5773 AAAGGAAACCTGTGAAGAGTCCGCGCATGAACCAACCGGAGCCGCTCCACTCCGC 5832
| | | | |
QY 5683 AGCAGCCCAACAGAGGAGCCCAACCCAGTACACAGAGCATACCAAGCGCGTGGCC 5742
| | | | |
Db 5833 AGCAGCCCAACAGAGGAGCCCAACCCAGTACACAGAGCATACCAAGCGCGTGGCC 5892
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| | | | |
Db 5893 TCAGCCCAAGCGCGCGCCGAGAGCCCAAGCCAGCCAGAGCCAGAGCAACCCACCGC 5952
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| | | | |
Db 6013 GAGAAATCCCGCGCGGATGCTCAGACAGCGGAGAGCGGTCCCGGGAGAGCTGTTT 6072
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| | | | |
Db 6073 GAAAGCAGCAGCAGAGGCGCGCTGCTGCGGAGCCGAGAGCCCGCTGTCCAGGTTG 6132
| | | | |
QY 5983 AACAAAGGAGAGGCGAGAGTGTCTTCAAGTTTACGTTAACATGTGACCT 6037
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RESULT 11
US-10-262-511-1
; Sequence 1, Application US/10262511
; Publication No. US2004003823A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Miller, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Rameeh
; APPLICANT: Ju, Jinfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zethusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Carterton, Bina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.

APPLICANT: Shenoy, Suresh G.
APPLICANT: Shimkete, Richard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,435
PRIOR FILING DATE: 2001-10-05
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuroSeqList version 0.1
SEQ ID NO 1
LENGTH: 6189
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(6159)
US-10-262-511-1

Query Match 91.4%; Score 5631; DB 17; Length 6189;
Best Local Similarity 95.3%; Pired. No. 0;
Matches 5944; Conservative 0; Mismatches 45; Indels 246; Gaps 4;

QY 1 ATGTTGAAGTTCAATATGAGCGCGAAATCTTTGATGCTGCTGCTGAACCAT 60
DB 1 ATGTTGAAGTTCAATATGAGCGCGAAATCTTTGATGCTGCTGCTGAACCAT 60
QY 61 GCCAGCGGGGCTTCAAGGCTGAATCTGTTCTTCCAGGGGAAACCACTTTATGACTCA 120
DB 61 GCCAGCGGGGCTTCAAGGCTGAATCTGTTCTTCCAGGGGAAACCACTTTATGACTCA 120
QY 121 CAGCAGATGCTCTCTCTTTCCGAGAAAGGATATTAGATGCCCTTTTGTCTCTTTGAA 180
DB 121 CAGCAGATGCTCTCTCTTTCCGAGAAAGGATATTAGATGCCCTTTTGTCTCTTTGAA 180
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DB 121 CAGCAGATGCTCTCTCTTTCCGAGAAAGGATATTAGATGCCCTTTTGTCTCTTTGAA 180
QY 181 GAATGAGTCAGGCTGCTGATGAGATTAAAGCAGTGAGCAACTTTTGTCCGGAAGTAT 240
DB 181 GAATGAGTCAGGCTGCTGATGAGATTAAAGCAGTGAGCAACTTTTGTCCGGAAGTAT 240
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DB 301 AGCTTGTAGTGTGTGTCTTTGAGATGCAAGTGTATAGAGAAAGCAACCGG 360
QY 361 GACATCTATGCTTGAAGTGAAGAAAGGCTTTATTTGGCCAGAGAGGTTTCA 420
DB 361 GACATCTATGCTTGAAGTGAAGAAAGGCTTTATTTGGCCAGAGAGGTTTCA 420

QY 421 TTTTGGAGAGAGCGGAACAATATATCTGAAGCAAGCCCGGATCCCAATTA 480
DB 421 TTTTGGAGAGAGCGGAACAATATATCTGAAGCAAGCCCGGATCCCAATTA 480
QY 481 CAGTATGCTTTCAGGACAAATAATCACTTTATCTGATGAGGAAATATGAGCTGAGG 540
DB 481 CAGTATGCTTTCAGGACAAATAATCACTTTATCTGATGAGGAAATATGAGCTGAGG 540
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DB 661 GACATCAAGCTGAGAACATCTCGTTGACCGCACAGACATCAAGCTGTGTGATTTT 720
QY 721 GGATCTGCCGGAATGAATTCAAACAAGATGTGAATGCCAACTCCGATTTGGAC 780
DB 721 GGATCTGCCGGAATGAATTCAAACAAGATGTGAATGCCAACTCCGATTTGGAC 780
QY 778 CCAATTAATGATGCTCTGATGCTGATGATGATGATGATGATGATGATGATGATGAT 840
DB 778 CCAATTAATGATGCTCTGATGCTGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 GGCTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 900
DB 841 GGCTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 900
QY 901 TCCCTCTTGCAGAGGAACTCTGCGAGAACCTTCAATTAATTAATTAATTAATTAAT 960
DB 901 TCCCTCTTGCAGAGGAACTCTGCGAGAACCTTCAATTAATTAATTAATTAATTAAT 960
QY 961 TTTTGAATTTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
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QY 1021 TTGTTGCGGCGCAGAAAGAGACTGAAGTTGAAGTCTTTTGTGCTGATCTTTCTTC 1080
DB 1021 TTGTTGCGGCGCAGAAAGAGACTGAAGTTGAAGTCTTTTGTGCTGATCTTTCTTC 1080
QY 1078 TCTAAATTTGATGAGCAATTCGTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1137
DB 1078 TCTAAATTTGATGAGCAATTCGTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1137
QY 1141 TCTGAGATGACATCTTCAATTTTGAATGAACAGAGAAATTCGAGGTTTCAATCTCT 1200
DB 1141 TCTGAGATGACATCTTCAATTTTGAATGAACAGAGAAATTCGAGGTTTCAATCTCT 1200
QY 1138 TCTGAGATGACATCTTCAATTTTGAATGAACAGAGAAATTCGAGGTTTCAATCTCT 1197
DB 1138 TCTGAGATGACATCTTCAATTTTGAATGAACAGAGAAATTCGAGGTTTCAATCTCT 1197
QY 1201 CCGTCCAGCTGAGCCCTCAGGCTTCTGAGGTAAGAACTGCGGTTTGTGGGTTTTCG 1260
DB 1201 CCGTCCAGCTGAGCCCTCAGGCTTCTGAGGTAAGAACTGCGGTTTGTGGGTTTTCG 1260
QY 1198 CCGTCCAGCTGAGCCCTCAGGCTTCTGAGGTAAGAACTGCGGTTTGTGGGTTTTCG 1257
DB 1198 CCGTCCAGCTGAGCCCTCAGGCTTCTGAGGTAAGAACTGCGGTTTGTGGGTTTTCG 1257
QY 1261 TACAGCAAGCACTGGGATTTCTTGTGATCTGATCTGTTGTGTGAGGTTTGAATCT 1320
DB 1261 TACAGCAAGCACTGGGATTTCTTGTGATCTGATCTGTTGTGTGAGGTTTGAATCT 1320
QY 1258 TACAGCAAGCACTGGGATTTCTTGTGATCTGATCTGTTGTGTGAGGTTTGAATCT 1317
DB 1258 TACAGCAAGCACTGGGATTTCTTGTGATCTGATCTGTTGTGTGAGGTTTGAATCT 1317
QY 1321 CCGTCCAGCTGAGCCCTCAGGCTTCTGAGGTAAGAACTGCGGTTTGTGGGTTTTCG 1380
DB 1321 CCGTCCAGCTGAGCCCTCAGGCTTCTGAGGTAAGAACTGCGGTTTGTGGGTTTTCG 1380
QY 1318 CCGTCCAGCTGAGCCCTCAGGCTTCTGAGGTAAGAACTGCGGTTTGTGGGTTTTCG 1377
DB 1318 CCGTCCAGCTGAGCCCTCAGGCTTCTGAGGTAAGAACTGCGGTTTGTGGGTTTTCG 1377
QY 1381 TCTCAGGACAGTGTCAACAAGTGAAGAGAGAAATGACCGGTTTATCTGAGAGTGTCA 1440
DB 1381 TCTCAGGACAGTGTCAACAAGTGAAGAGAGAAATGACCGGTTTATCTGAGAGTGTCA 1440
QY 1441 GAGGTGAGGCTGTGTTTATGATGAAGAGAGTGAAGCTGAGGCTTGAAGTCAAG 1500
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QY 1438 GAGGTGAGGCTGTGTTTATGATGAAGAGAGTGAAGCTGAGGCTTGAAGTCAAG 1497
DB 1438 GAGGTGAGGCTGTGTTTATGATGAAGAGAGTGAAGCTGAGGCTTGAAGTCAAG 1497

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QY	1561	TTGGAGCAGACCGGATGGAGGTGTCCAGAGGAGTGA CAAGCACTGACGCTTCAT	1620
Db	1558	TTGGAGCAGACCGGATGGAGGTGTCCAGAGGAGTGA CAAGCACTGACGCTTCAT	1617
QY	1621	GATATCAGAGACAGAGCCGAGAGCTCCAGAAATCAAGAGCAGAGATACAGGCTCA	1680
Db	1618	GATATCAGAGACAGAGCCGAGAGCTCCAGAAATCAAGAGCAGAGATACAGGCTCA	1677
QY	1661	GTGGAAGAAATGAGGTTGATGATGATCA GTTGGAAGAGATCTTGTCTCAGCAAGAA	1740
Db	1678	GTGGAAGAAATGAGGTTGATGATGATCA GTTGGAAGAGATCTTGTCTCAGCAAGAA	1737
QY	1741	CGGAGTGATCTCTACGATCTGAGCTGAGAGATCTCGGCTTGTGCTGAAAGATTCAG	1800
Db	1738	CGGAGTGATCTCTACGATCTGAGCTGAGAGATCTCGGCTTGTGCTGAAAGATTCAG	1797
QY	1801	CGGAAGCGCAGAGATGTCAAGATTAATCTGTTGAAGCTAAAGATCAAGGAGAGCTGAA	1860
Db	1798	CGGAAGCGCAGAGATGTCAAGATTAATCTGTTGAAGCTAAAGATCAAGGAGAGCTGAA	1857
QY	1861	GTGGAGAAATTCGAAATCTGAGAGAGATCAATGCTGAGCAGCAGCTCAAAATTCAGAG	1920
Db	1858	GTGGAGAAATTCGAAATCTGAGAGAGATCAATGCTGAGCAGCAGCTCAAAATTCAGAG	1917
QY	1921	CTCCAAAGGAAACTGGAAGAGGCTG-----	1945
Db	1918	CTCCAAAGGAAACTGGAAGAGGCTGTTAAAGCCAGACCGAGGCGCACCGAGCTGTCAG	1977
QY	1946	-----CAAGAGCCGAGCCGAGAGGGAGCTGGAAGCTGCAAAACCGAGAG	1992
Db	1978	AATATCCGCGCAGGCAAGAGACGAGCCGAGAGGGAGCTGGAAGAGCTGCAAAACCGAGAG	2037
QY	1993	GATTCCTTGTGAAGGCATAGAAAGAGCTGTGGAAGCTTGAGAAACGCGCCGATTCCTGTG	2052
Db	2038	GATTCCTTGTGAAGGCATAGAAAGAGCTGTGGAAGCTTGAGAAACGCGCCGATTCCTGTG	2097
QY	2053	GAGAACAAAGTAAGAGACTAGAGACCACTGAGGGGTGAGAAACAAGCTGAAAGATGAC	2112
Db	2098	GAGAACAAAGTAAGAGACTAGAGACCACTGAGGGGTGAGAAACAAGCTGAAAGATGAC	2157
QY	2113	ATCCAGACAAATCCCAACAGATCCAGCAGATGCTGTGATTAATTTCTGAGCTCGAAGAG	2172
Db	2158	ATCCAGACAAATCCCAACAGATCCAGCAGATGCTGTGATTAATTTCTGAGCTCGAAGAG	2217
QY	2173	AAACATGGGAGGCCCAAGTCTCAGCCGACGACCTGAAATGTCATTGAAACAGAAAGAG	2232
Db	2218	AAACATGGGAGGCCCAAGTCTCAGCCGACGACCTGAAATGTCATTGAAACAGAAAGAG	2277
QY	2233	CAGACCTATGAGGAAAGATTTAAAGTGTGGAACATCAGATTAAGAAAGACTTGCTGAC	2292
Db	2278	CAGACCTATGAGGAAAGATTTAAAGTGTGGAACATCAGATTAAGAAAGACTTGCTGAC	2337
QY	2293	AAGGAGACATCTGAGGAACATGATCCAGAGACAGCAGAGGAGGGCCCATGGAAGGGCAAA	2352
Db	2338	AAGGAGACATCTGAGGAACATGATCCAGAGACAGCAGAGGAGGGCCCATGGAAGGGCAAA	2397
QY	2353	ATTCTCAGCGAACAGAGGCGATATCAATGCTATGGAATTCGAAGATCAATGCCCTGAAA	2412
Db	2398	ATTCTCAGCGAACAGAGGCGATATCAATGCTATGGAATTCGAAGATCAATGCCCTGAAA	2457
QY	2413	CAGAGGATGTTGGAACTGTCTGAAGCCCAATTAATTGTGACGAAATATGACGCTTTTAAAC	2472
Db	2458	CAGAGGATGTTGGAACTGTCTGAAGCCCAATTAATTGTGACGAAATATGACGCTTTTAAAC	2517
QY	2473	CAAGAGAACATGAAGGCCCAAGAGAGATGATTTCTGAACTCAGGCAACGAAATTTTAC	2532
Db	2518	CAAGAGAACATGAAGGCCCAAGAGAGATGATTTCTGAACTCAGGCAACGAAATTTTAC	2577
QY	2533	CTGAGAGCACAGGCTGGGAAGTTGGAGGCCAGAACCGAAACTGAGAGAGCAGCTGGAG	2592

Db	2578	CTGGAGACACAGGCTGGGAGATTGGAGGCCAGAAACCAAAACTGGAGAGCAGCTGGAG	263
Qy	2593	AAGATCAGCAGCACCAAGACCAACAGTGAACAAGATCGGCTGGAGACTGGAGCAAGATTG	265
Db	2638	AAGATCAGCAGCAAGACCAACAGTGAACAAGATCGGCTGGAGACTGGAGCAAGATTG	269
Qy	2653	CGGAGAGTCAGTCTAGAGCACAGAGAGCAGAACTGGAGCTCAAGCGCAGCTCAAGAG	271
Db	2698	CGGAGAGTCAGTCTAGAGCACAGAGAGCAGAACTGGAGCTCAAGCGCAGCTCAAGAG	275
Qy	2713	CTACAGCTCTCCCTTCAGAGCGCGAGTCAAGTTTGACAGCCCTTCAGAGCTTCAGCGCG	277
Db	2758	CTACAGCTCTCCCTTCAGAGCGCGAGTCAAGTTTGACAGCCCTTCAGAGCTTCAGCGCG	281
Qy	2773	GGCCCTGGAGAGCGCAGCTTCGCGCAGCGGAGACAGAGCTGGAGAGAGACCAACAGCAACT	283
Db	2818	GGCCCTGGAGAGCGCAGCTTCGCGCAGCGGAGACAGAGCTGGAGAGAGACCAACAGCAACT	287
Qy	2833	GAAGAGAGATTCACAGGCATCAACGCGCATATAGAGTGAATTCAGCGCAAAATTTGATCT	289
Db	2878	GAAGAGAGATTCACAGGCATCAACGCGCATATAGAGTGAATTCAGCGCAAAATTTGATCT	293
Qy	2893	CTTCGTAACAGCTGTACTGTATATCACAGCTTGAAGAGCAGCTAAACAGCTGACGAG	295
Db	2938	CTTCGTAACAGCTGTACTGTATATCACAGCTTGAAGAGCAGCTAAACAGCTGACGAG	299
Qy	2953	GACAAAGCTGAATCTCAACAAACAAACCTTCAATCTTGTCCAAACAACTGATGAGGCTTCT	301
Db	2998	GACAAAGCTGAATCTCAACAAACAAACCTTCAATCTTGTCCAAACAACTGATGAGGCTTCT	305
Qy	3013	GGCGCCAAACGACGAGATTGTACAACTGGAGAGTGAAGTGCACATCTCCGCGGAGATC	307
Db	3058	GGCGCCAAACGACGAGATTGTACAACTGGAGAGTGAAGTGCACATCTCCGCGGAGATC	311
Qy	3073	ACGGAGAGAGATTCAGCTTACCAAGCCAGAACAAACGATGAGGCTTGAAGCCAGC	313
Db	3118	ACGGAGAGAGATTCAGCTTACCAAGCCAGAACAAACGATGAGGCTTGAAGCCAGC	317
Qy	3133	TGCACCAATGCTGGAGAGAAACAGGTACATGATTTGAGAGGCCCTAAACGATGACCTGCTAAG	319
Db	3178	TGCACCAATGCTGGAGAGAAACAGGTACATGATTTGAGAGGCCCTAAACGATGACCTGCTAAG	323
Qy	3193	AAAGAGCGGACGATGGGAGGCTTCGAGAGAGGCTCTCGGGTGTATGAGAAATCCAGATTGAG	325
Db	3238	AAAGAGCGGACGATGGGAGGCTTCGAGAGAGGCTCTCGGGTGTATGAGAAATCCAGATTGAG	329
Qy	3253	TGTGGGTTTGGAGAGCTTCAGAGATGCTTGACACCGAGAAACAGAGCAGGGCGAGAGCC	331
Db	3298	TGTGGGTTTGGAGAGCTTCAGAGATGCTTGACACCGAGAAACAGAGCAGGGCGAGAGCC	335
Qy	3313	GATCAGCGGATCAACCGAGTCTCCGCGCAGGTGGTGGAGCTTCGGAGTGAAGAGACCAAGGCT	337
Db	3358	GATCAGCGGATCAACCGAGTCTCCGCGCAGGTGGTGGAGCTTCGGAGTGAAGAGACCAAGGCT	341
Qy	3373	GAGATTCTCGCTTCGACAGCAGGCTCTCAAAAGACAGAACTGGAAGGCCGAGAGGCTCTCT	343
Db	3418	GAGATTCTCGCTTCGACAGCAGGCTCTCAAAAGACAGAACTGGAAGGCCGAGAGGCTCTCT	347
Qy	3433	GACAAGCTCAATGACTTGGAGAGAAAGCATGTATGCTTGAATGAATGCCGAGGCTTA	349
Db	3478	GACAAGCTCAATGACTTGGAGAGAAAGCATGTATGCTTGAATGAATGCCGAGGCTTA	353
Qy	3493	CAGCAGAAAGCTGGAGACTGAACAGAGACTCAAAACAGAGGCTTCGGAGAGAGCAAGCCAAA	355
Db	3538	CAGCAGAAAGCTGGAGACTGAACAGAGACTCAAAACAGAGGCTTCGGAGAGAGCAAGCCAAA	359
Qy	3553	TTACAGCAGCAGATGGAAGCTTCGACAGAAATCAATTTTCCGTCTGAGCTCAAGAGCTGCAA	361
Db	3598	TTACAGCAGCAGATGGAAGCTTCGACAGAAATCAATTTTCCGTCTGAGCTCAAGAGCTGCAA	365
Qy	3613	GAAGCTCTAGATCGGGCTGATCTTACTGAAGACAGAAAGAAAGTGACTTGGAGTATCAGCTG	367

Db 3658 GAAGCTAGATCGGGCTGATCTACTGAAAGACAGAAAAGAAAGTGACTTGGAGTATCAGCTG 3717
Qy 3673 GAAAAATTCAAGTTTCTTAATTCTCATGAAAAGGTGAAAATGGAAGGCACTATTTCCTCA 3732
Db 3718 GAAACATTCAAGGTGCTTAATCTCATGAAAAGGTGAAAATGGAAGGCACTATTTCCTCA 3777
Qy 3733 CAACCAAACTCATGATTTTTCGAAAGCAAAAATGGAACCACTGCTAAAAAGAAAAG 3792
Db 3778 CAACCAAACTCATGATTTTTCGAAAGCAAAAATGGAACCACTGCTAAAAAGAAAAG -- 3835
Qy 3793 GGTATTTATTTAGTCAGCGAAAGAGACCTGCTTTACCAACAGGTTCTCTCAGATAC 3852
Db 3836 -----AGGTGCTCTGCAGTAC 3852
Qy 3853 AATGAGCTGAAGTGGCCCTTGAGAAAGAAAGAGAAAGTCTGCTGTGCAAGCTTAAGAAAGCC 3912
Db 3853 AATGAGCTGAAGTGGCCCTTGAGAAAGAAAGAGAAAGTCTGCTGTGCAAGCTTAAGAAAGCC 3912
Qy 3913 CTTCAAGAGACCCGCAATCGAGCTCCGGTCCGCCGGAGAGAGCTGCCACCGCAAAAGCA 3972
Db 3913 CTTCAAGAGACCCGCAATCGAGCTCCGGTCCGCCGGAGAGAGCTGCCACCGCAAAAGCA 3972
Qy 3973 ACGGACACCCACACCCATTCACGCGACGCAACCGGAGGAGAGATGCGCATGTCCGCC 4032
Db 3973 ACGGACACCCACACCCATTCACGCGACGCAACCGGAGGAGAGATGCGCATGTCCGCC 4032
Qy 4033 ATGTGCGGTCCGCAAGACACAGCCCAATGACCTGCTGCTGCGCCCGCATTCAGC 4092
Db 4033 ATGTGCGGTCCGCAAGACACAGCCCAATGACCTGCTGCTGCGCCCGCATTCAGC 4092
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Db 4093 CGGAGAAAGAGTCTCAACTCGAGAGAAATTTAGTCCGGTCTTAAAGAAAGCATGCAAC 4152
Qy 4153 CAACAATATTCTCTCAACCGATTCAACGTAGACATGAGCATGCGAGCCCAAAAGTGTGCTG 4212
Db 4153 CAACAATATTCTCTCAACCGATTCAACGTAGACATGAGCATGCGAGCCCAAAAGTGTGCTG 4212
Qy 4213 TGTCTGGAATACCTGTGCACTTTTGAAGCGCAGGCAATCCAAATGTCTCGAATGTCAAGTGA 4272
Db 4213 TGTCTGGAATACCTGTGCACTTTTGAAGCGCAGGCAATCCAAATGTCTCGAATGTCAAGTGA 4272
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Qy 4453 GAGCAGCAAGGCTGGGACAGGAAGTACATTTGCTGAGGGGATCAAAAGTCTCATTTAT 4512
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Qy 4513 GACAAATGAAGCCAGAGAGCTGGAAGAGGCGGTGAAGAAATTTGAGCTGTCTCTCC 4572
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Qy 4573 GACGGGGAATGATCTATTCTATTCATGTGCGGTGCTTCCGAATCTCCAAATACAGCCAA 4632
Db 4573 GACGGGGAATGATCTATTCTATTCATGTGCGGTGCTTCCGAATCTCCAAATACAGCCAA 4632
Qy 4633 GCA----- 4635
Db 4633 GCAAGATGCCCATATCATCTGAAGATGAATCTCACCCGACACACCTGCTGAGCCGGG 4692
Qy 4636 ----- 4635
Db 4693 AGAACCTTACTTGTAGCTCCAGGTTCTCTGACAAACAGGCGTGGGTCAACGACCTTA 4752

Qy 4636 -----GAAAAAGCAGAGCTGATGCTAAACTG 4662
Db 4753 GAATCATGTTGCGAGGTGGAGAGTTTCTAGAGAAAAGACAGAGCTATGCTTAACAG 4812
Qy 4663 CTTGGAATCTCCCTGTGTAACCTGGAAGGTGATGACCGTCTAGACATGAACTGACGCTG 4722
Db 4813 CTTGGAATCTCCCTGTGTAACCTGGAAGGTGATGACCGTCTAGACATGAACTGACGCTG 4872
Qy 4723 CCGTTCAGTGACCAAGGTGTTGTTGGGACCCGAGAAAGGCTCTACGCTGAAATGTC 4782
Db 4873 CCGTTCAGTGACCAAGGTGTTGTTGGGACCCGAGAAAGGCTCTACGCTGAAATGTC 4932
Qy 4783 TTGAAAAATCTCCCTTAACCCATGCTCCAGGAATTTGAGCGCTTCCAAATTTATATATC 4842
Db 4933 TTGAAAAATCTCCCTTAACCCATGCTCCAGGAATTTGAGCGCTTCCAAATTTATATATC 4992
Qy 4843 AAGGACCTGGAAGAGCTACTCATGATAGCAGGAGAAAGCGGCACTGTGCTTGTGAC 4902
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Qy 4903 GTGAAGAAAGTGAACAGTCCCTGGCCAGTCCACCTGCTGCCAGCCGACATCTCA 4962
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Db 5173 GGGCTCTGATCTGTGACAGCCATGCGCAGCAAAAGTGTGATTTCTCGTACAAAGAAAC 5232
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Db 5233 CTGAGCAATCTGCACTCCGAAAGAGATGAGACTCAGAGCCCTGCACTGTATCCAC 5292
Qy 5143 TTCAACCAATTAAGTATCTCATTTGGAACCAATTAATTTAGAAATGCAATGAAGAG 5202
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Qy 5203 TACAGCTCTGAGGAATCTCTGATTAAGATGACAAATCTCTGAGCACTGCTGTGTTGCC 5262
Db 5353 TACAGCTCTGAGGAATCTCTGATTAAGATGACAAATCTCTGAGCACTGCTGTGTTGCC 5412
Qy 5263 GCTCTTCCAAAGCTTCTCTGATCTGATCTGCAAGTGAACAGCGGCGAGCGAGAG 5322
Db 5413 GCTCTTCCAAAGCTTCTCTGATCTGATCTGCAAGTGAACAGCGGCGAGCGAGAG 5472
Qy 5323 GAGTACTTGTGTTTCCAGAAATTTGGAAGTTCGTGGAATTTCTTAAGGAAGAGCTAGC 5382
Db 5473 GAGTACTTGTGTTTCCAGAAATTTGGAAGTTCGTGGAATTTCTTAAGGAAGAGCTAGC 5532
Qy 5383 CCGACAGAGATCTCAAGTGAAGTGGCTTACCTTTGGCTTTGCTCAAGAAACCTTAT 5442
Db 5533 CCGACAGAGATCTCAAGTGAAGTGGCTTACCTTTGGCTTTGCTCAAGAAACCTTAT 5592
Qy 5443 CTGTTTGTGACCCACTTCAACTCACTCGAAGTAAATTTGAGATCCAGGCAAGCTTCA 5502
Db 5593 CTGTTTGTGACCCACTTCAACTCACTCGAAGTAAATTTGAGATCCAGGCAAGCTTCA 5552
Qy 5503 GGGACCCCTGCGCGAGCGTACCTGGAACATCCCGAAGCCGCGCTACCTGGGCGCTGCATT 5562
Db 5553 GGGACCCCTGCGCGAGCGTACCTGGAACATCCCGAAGCCGCGCTACCTGGGCGCTGCATT 5712
Qy 5563 TCTCAGAGAGATTTACTTGGCGTCTCTCATACAGATTAATTAAGGCTCATTTGCTGC 5622
Db 5713 TCTCAGAGAGATTTACTTGGCGTCTCTCATACAGATTAATTAAGGCTCATTTGCTGC 5772
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Db 5773 AAGGGAACCTGCTGAAGAGATCCGCACTGAACACACCGGAGGCGCTGCACTCCGC 5832

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QY	5743	TCGAGCCGAGCGCCGCGCCGAAAGGCCCAACCCGACAGAGCCAGACACCCACCGC	5802
Db	5893	TCGAGCCGAGGCGCCGCGAAAGGCCCCGACGACCCGCGAGAGCCAAAGACACCCACCGC	5952
QY	5803	TACCGCAGAGGGGCGGACCGAGGTGGCGGGAACAAGTCCCTGGCGCGGCCCTGAGAGGA	5862
Db	5953	TACCGCAGAGGGGCGGACCGAGCTGGCGAGGACAAAGTCCCTGGCGCGGCCCTGAGAGGA	6012
QY	5863	GAGAAATCCCCCGGCGGATGCTACGACGCGGAGAGAGCGATCCCCCGGAGGCGTGT	5922
Db	6013	GAGAAATCCCCCGGCGGATGCTACGACGCGGAGAGAGCGATCCCCCGGAGGCGTGT	6072
QY	5923	GAAAGCAGACAGAGGCGCGGCTGGCTGCGGAGAGCGGAGAACCCGCTGCCAGGTG	5982
Db	6073	GAAAGCAGACACAGAGGCGCGGCTGGCTGCGGAGAGCGGAGAACCCGCTGCCAGGTG	6132
QY	5983	AACAAGGAAAGGGCGAGATGCTCTCAAGTTTCAACGTTAAACATGTACCT	6037
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RESULT 12

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; Sequence 8, Application US/09964956
; Publication No. US20040043926A1
; GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glenda
; APPLICANT: Miller, Isabelle
; APPLICANT: Sidne, David
; APPLICANT: Gutther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Gibbs, William M
; APPLICANT: Albrock II, John P
; APPLICANT: Lebley, Denise M
; APPLICANT: Burgess, Catherine B
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leach, Martin D
; APPLICANT: Shmukets, Richard A
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; FILE REFERENCE: 21402-124
; CURRENT APPLICATION NUMBER: US/09/964,956
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,631
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; PRIOR APPLICATION NUMBER: 60/235,808
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; PRIOR APPLICATION NUMBER: 60/236,064
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; PRIOR APPLICATION NUMBER: 60/238,399
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,396
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/276,667

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? PRIOR FILING DATE: 2001-05-31
? PRIOR APPLICATION NUMBER: 60/304,866
? PRIOR FILING DATE: 2001-07-12
? NUMBER OF SEQ ID NOS: 127
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 8
? LENGTH: 6201
? TYPE: DNA
? ORGANISM: Homo sapiens
US-03-964-956-8

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Query Match	91.4%;	Score 5629.8;	DB 11;	Length 6201;
Best Local Similarity	95.7%;	Pred. No. 0;		
Matches 5929;	Conservative 0;	Mismatches 22;	Indels 246;	Gaps 4

QY	ANGTTGAAGTTCAAAATATAGAGACGGGGAATCCCTTTGAAATGCTGAGTCTGTCGAACCCCAAT	60
Db	1 ANGTGTAAAGTTCAAAATATAGAGACGGGGAATCCCTTTGAAATGCTGAGTCTGTCGAACCCCAAT	60
QY	61 GCCAGCCGGGCTCCAGGCTGATCTGTCTTCACAGGGGAAACACCCCTTATGACTCAA	120
Db	61 GCCAGCCGGGCTCCAGGCTGATCTGTCTTCACAGGGGAAACACCCCTTATGACTCAA	120
QY	121 CAGCAGATGTCTCTCTCTTTCCCGAGAAAGGATATTAGATGCCCTCTTTGTCTCTTTGAA	180
Db	121 CAGCAGATGTCTCTCTCTTTCCCGAGAAAGGATATTAGATGCCCTCTTTGTCTCTTTGAA	180
QY	181 GAATGACATGACGCTGCTCTGATGAAAGTTAAGACGAGACGAATTTGTCCGGAAGAT	240
Db	181 GAATGACATGACGCTGCTCTGATGAAAGTTAAGACGAGACGAATTTGTCCGGAAGAT	240
QY	241 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTGGCAAAAGCATTCGAAGTCA	300
Db	241 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTGGCAAAAGCATTCGAAGTCA	300
QY	301 AGTCTTTAGGTTGTGTGTCACTTTGCTGAATGCAAGTGTGTATAGAGAAAGCAACCGGG	360
Db	301 AGTCTTTAGGTTGTGTGTCACTTTGCTGAATGCAAGTGTGTATAGAGAAAGCAACCGGG	360
QY	361 GACATCTATGCTATGAAGATGATGAAGAAAGGCTTATTTGGCCACAGACAGAGTTTCA	420
Db	361 GACATCTATGCTATGAAGATGATGAAGAAAGGCTTATTTGGCCACAGACAGAGTTTCA	420
QY	421 TTTTGTGAGAAAGCCGGAACATATTATCTGAAAGCACAAAGCCCGTGATCCCCCAATTA	480
Db	421 TTTTGTGAGAAAGCCGGAACATATTATCTGAAAGCACAAAGCCCGTGATCCCCCAATTA	480
QY	481 CAGTATGCTTTCAAGAACAAAATCACCTTTATCTGATGAGAGAAATCAGCCTGAGAGG	540
Db	481 CAGTATGCTTTCAAGAACAAAATCACCTTTATCTGATGAGAGAAATCAGCCTGAGAGG	540
QY	541 GACTTGCTGTCACTTTTGATATAGATGAGGACCAAGTTAGATGAAAAACCTGATCAAGTTT	600
Db	541 GACTTGCTGTCACTTTTGATATAGATGAGGACCAAGTTAGATGAAAAACCTGATCAAGTTT	600
QY	601 TACCTAGCTGAGTATTTTGGCTGTTCACAGCGTTCACTGATGGGATACGTGCATCGA	660
Db	601 TACCTAGCTGAGTATTTTGGCTGTTCACAGCGTTCACTGATGGGATACGTGCATCGG	660
QY	661 GACATCAAGCTGAGAACATTTCTGTGTGACCGCACAGACACATCAAGCTGTGTGATTTT	720
Db	661 GACATCAAGCTGAGAACATTTCTGTGTGACCGCACAGACACATCAAGCTGTGTGATTTT	720
QY	721 GGATCTGCGCGGAAATGAATTCAAACAAAGATGTGTGAATGCCAAATCCCGATTGGGAGCC	780
Db	721 GGATCTGCGCGGAAATGAATTCAAACAA--GATGAATGCCAAATCCCGATTGGGAGCC	777
QY	781 CCAAGATTACATGAGCTCTCTGAAGTCTGATCTGTGATGAACGGGGAATGGAAGACCACTTAC	840
Db	778 CCAATATTACATGAGCTCTCTGAAGTCTGATCTGTGATGAACGGGGAATGGAAGACCACTTAC	837

QY	841	GGCTCGAGACTGTCAGTCGGTGGTCAGTGGGCGCTGATATGCTCTATGAGATGATATTTATGGGAGA	900
Db	838	GGCCCTCGAGACTGTGACTGGTGGTCAGTGGGCGCTGATATGCTCTATGAGATGATATTTATGGGAGA	897
QY	901	TCGCCCTTCGAGAGGGAACCTCTGCGCAAGAACCTTCAATTAACATATATGAATTTCCAGCGG	960
Db	898	TCGCCCTTCGAGAGGGAACCTCTGCGCAAGAACCTTCAATTAACATATATGAATTTCCAGCGG	957
QY	961	TTTTTGAATAATTCAGATGAGACCCCAAGGTGAGCAGTGTACTTTCTTGATCTGATTTCAAGC	1020
Db	958	TTTTTGAATAATTCAGATGAGACCCCAAGGTGAGCAGTGTACTTTCTTGATCTGATTTCAAGC	1017
QY	1021	TTGTGTGCGGCGCAGAAAAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCTCTTCTTC	1080
Db	1018	TTGTGTGCGGCGCAGAAAAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCTCTTCTTC	1077
QY	1081	TCCTAAATTTGACTGGAAACAATTGTGTAATCTCTCCCTCCCTCGTTCCCAACCTCAAG	1140
Db	1078	TCCTAAATTTGACTGGAAACAATTGTGTAATCTCTCCCTCCCTCGTTCCCAACCTCAAG	1137
QY	1141	TCGTACGATGACACCTCCCAATTTTATGTAACACAGAGAAGAAATCGTGGGTTTCACTCTCT	1200
Db	1138	TCGTACGATGACACCTCCCAATTTTATGTAACACAGAGAAGAAATCGTGGGTTTCACTCTCT	1197
QY	1201	CCGTGCCAGCTGAGGCCCTCTCAGGCTCTTCGAGTGAAAGACTGCGGTTGTGGGAGTTTTCG	1260
Db	1198	CCGTGCCAGCTGAGGCCCTCTCAGGCTCTTCGAGTGAAAGACTGCGGTTGTGGGAGTTTTCG	1257
QY	1261	TACAGCAAGGCACTGGGGATTTCTTGCTGATATCTGATGCTGTGTGTGTGCGGCTCTGGACTCC	1320
Db	1258	TACAGCAAGGCACTGGGGATTTCTTGCTGATATCTGATGCTGTGTGTGTGCGGCTCTGGACTCC	1317
QY	1321	CCTGCGCAAGACTGAGCTCCATGGAAGAAACCTTCTCATCAAAAGCAAAAGACTCTCAAGAC	1380
Db	1318	CCTGCGCAAGACTGAGCTCCATGGAAGAAACCTTCTCATCAAAAGCAAAAGACTCTCAAGAC	1377
QY	1391	TCTCAGGACAAGCTGTCAACAAGTGGAGCAGAGAAATGACCCGGTTATCATCGAGAGTGTCA	1440
Db	1378	TCTCAGGACAAGTGTCAACAAGTGGAGCAGAGAAATGACCCGGTTATCATCGAGAGTGTCA	1437
QY	1441	GAGGTGAGAGCTGTGCTTATGTCAGAAAGAGGTGGAGCTGAAAGGCTCTGAGACTCAAGAA	1500
Db	1438	GAGGTGAGAGCTGTGCTTATGTCAGAAAGAGGTGGAGCTGAAAGGCTCTGAGACTCAAGAA	1497
QY	1501	TCCCTCTCTGAGCAGAGACCTTGCTCACTACATCAGAGAATGAGTGAAGCTTTAAAGGAAGT	1560
Db	1498	TCCCTCTCTGAGCAGAGACCTTGCTCACTACATCAGAGAATGAGTGAAGCTTTAAAGGAAGT	1557
QY	1561	TTGGAGCAAGCAGCAGATGGAGGTGTCCAGAGGAGTGTCAAAAGCACTGCAAGCTTCTCCAT	1620
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QY	1621	GATATCAGAGAGCAGAGCCCGGAAGCTCCAGAAATCAAAAGACAGAGACTCAAGGCTCAA	1680
Db	1618	GATATCAGAGAGCAGAGCCCGGAAGCTCCAGAAATCAAAAGACAGAGACTCAAGGCTCAA	1677
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Db	1678	GTGGAAGAAATGAGGTGTATATGTAATCAGTTGGAAGAGATCTTTGTCTCAGCAAGAA	1737
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Db	1738	CGAGATGATCTCTACGAATCTGAGCTGAGAGAGTCCGCTGTGCTGTGAGAAATTCAG	1797
QY	1801	CGGAAAGCGACAGAAATGTCAGATTAACCTGTTGAAGGCTTAAAGATCAAGGAAAGCTGAA	1860
Db	1798	CGGAAAGCGACAGAAATGTCAGATTAACCTGTTGAAGGCTTAAAGATCAAGGAAAGCTGAA	1857
QY	1861	GTGGGAGAAATATGCGAAACTGAGAGAAATCAATGCTGAGCAGCAGCTCAAAATTCAGGAG	1920
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2518	CAAAAGAACATGAAGGCCCAAGAAAGAGTGTATTCTGAAACTCAGGCAACAAATTTTAC	2577	
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2638	AAGATCAGCCACCAAGACCAAGTGAACAGAAATCGGCTGCGAACTGAGACAAAGATTG	2697	
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2938	CTTCGTAAACAGCTGTACTGTATATCAGACCTGAGAGAGCAGCTTAAACAGACTGACCGAG	2997	
2953	GACACGCTGAACCTCAACAAACCTTCTACTTGTCCAAACAACTGATGAGGCTTCT	3012	

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QY 3853 AATGAGCTGAAGCTGGCCCTGAGAAAGAAAGCTCGCTGTGACAGCTTAAGAGAGCC 3912
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GENERAL INFORMATION:
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APPLICANT: Miller, Isabelle
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APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Li, Li
APPLICANT: Guo, Xiaojia (Saasha)
APPLICANT: Paturajan, Meera
APPLICANT: Spytek, Kimberly A.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M.
APPLICANT: Ort, Tatiana
APPLICANT: Gorman, Linda
APPLICANT: Zernusen, Bryan D.
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Catterton, Elina
APPLICANT: Ji, Weizhen
APPLICANT: Miller, Charles E.
APPLICANT: Rastelli, Luca
APPLICANT: Stone, David J.
APPLICANT: Pena, Carol E. A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shinkets, Richard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
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PRIOR APPLICATION NUMBER: 60/381,038
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NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuroSeqList version 0.1
SEQ ID NO 13
LENGTH: 6201
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(6198)
US-10-262-511-13
Query Match 91.4%; Score 5629.8; DB 17; Length 6201;
Best Local Similarity 95.7%; Pred. No. 0;
Matches 5929; Conservative 0; Mismatches 22; Indels 246; Gaps 4;
QY 1 ATGTTGAAGTTCAATATAGAGCGGAGATCTTTGATGCTGCTGTAACCCATT 60
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QY 61 GCCAGCCGGGCTTCAGAGCTGAATCTGTTCTTCCAGGGGAAACCAACCTTTATGACTCAA 120
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DB 421 TTTTGAAGAGAGCGGAGACATATTTATCTCGAAGCAAGCCGCTGATCCCAATT 480
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DB 541 GACTGCTGCTCACTTTTGAATAGATATGAGAGACAGTATGATGAAGAAACCTGATACGTT 600
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RESULT 14
US-10-028-946-3
; Sequence 3, Application US/10028946
; Publication No. US20020123622A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Marcia
; APPLICANT: Fridde, Carl Johan
; TITLE OF INVENTION: No. US20020123622A1 Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0289-USA
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5877
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-028-946-3

Query Match 87.0%; Score 5358; DB 13; Length 5877;
Best Local Similarity 95.8%; Pred. No. 0;

Matches 5634; Conservative 0; Mismatches 5; Indels 243; Gaps 3;

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 QY 1681 GTGAG 1740
 Db 1681 GTGAG 1740
 QY 1741 CGAGTATCTTACGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
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 QY 1801 CGAG 1860
 Db 1801 CGAG 1860
 QY 1861 GTGAG 1920
 Db 1861 GTGAG 1920
 QY 1921 CTCAG 1944
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 QY 1945 -----GCAAG 1992
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 QY 1981 AATATCCGCAAG 2040
 Db 1981 AATATCCGCAAG 2040
 QY 1993 GATTTCTTGAAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2052
 Db 1993 GATTTCTTGAAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2052
 QY 2041 GATTTCTTGAAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2100
 Db 2041 GATTTCTTGAAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2100
 QY 2053 GAGAACAG 2112
 Db 2053 GAGAACAG 2112
 QY 2101 GAGAACAG 2160
 Db 2101 GAGAACAG 2160

2113 ATCCAGACAAAATCCCAAGATCCAGAGATGGCTGATATAAATTTCTGGAGCTCGAAG 2172
2161 ATCCAGACAAAATCCCAAGATCCAGAGATGGCTGATATAAATTTCTGGAGCTCGAAG 2220
2173 AAACATCGGAGGCCCAAGTCTCAGCCAGACCTTAAGATGCACTCTGAAAAGAAAAG 2232
2221 AAACATCGGAGGCCCAAGTCTCAGCCAGACCTTAAGATGCACTCTGAAAAGAAAAG 2280
2233 CAGCCTATAGAGAAAAGATTAAGTGTGACAAATCAGATTAAGAAACCTCGCTGAC 2292
2281 CAGCCTATAGAGAAAAGATTAAGTGTGACAAATCAGATTAAGAAACCTCGCTGAC 2340
2293 AAGGAGACACTGGAGAACATGATGACAGACACAGAGAGAGGCCCATGAGAAAGGCA 2352
2341 AAGGAGACACTGGAGAACATGATGACAGACACAGAGAGAGGCCCATGAGAAAGGCA 2400
2353 ATTCTCAGCGAAACAGAGGCGATGATCAATGCTATGGAATTCAGATCAGATCCCTGAA 2412
2401 ATTCTCAGCGAAACAGAGGCGATGATCAATGCTATGGAATTCAGATCAGATCCCTGAA 2460
2413 CAGAGATTTGTGAACATGCTGTAAGCCATAAATTGACCAATATGCACTCTTTTACC 2472
2461 CAGAGATTTGTGAACATGCTGTAAGCCATAAATTGACCAATATGCACTCTTTTACC 2520
2473 CAAAGGACATGAAAGGCCCAAGAGATGATTTCTGAATCTCAGGCAACAGAAATTTTAC 2532
2521 CAAAGGACATGAAAGGCCCAAGAGATGATTTCTGAATCTCAGGCAACAGAAATTTTAC 2580
2533 CTGGAGACACAGGCTGGGAAAGTTGAGGCCAGAACCGAAAACCTGAGAGACCTGGAG 2592
2581 CTGGAGACACAGGCTGGGAAAGTTGAGGCCAGAACCGAAAACCTGAGAGACCTGGAG 2640
2593 AAGATCAGCACCAAGACCAAGTGAAGAAATCGGCTGTGAAATTTGAGACAAATG 2652
2641 AAGATCAGCACCAAGACCAAGTGAAGAAATCGGCTGTGAAATTTGAGACAAATG 2700
2653 CGGAGAGTCACTAGAGACAGAGACAGAACTGAGCTCAAGCGCAGCTCACAGAG 2712
2701 CGGAGAGTCACTAGAGACAGAGACAGAACTGAGCTCAAGCGCAGCTCACAGAG 2760
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2761 CTACAGCTCTCCCTGCAAGAGCGCGAGTCAAGTTGACAGCCCTGCAAGCTGACCGGCG 2820
2773 GCCCTGAGAGCGCAGCTTGCCAGGCGAGACAGAGCTGAGAGACCAAGAGAGT 2832
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2941 CTTTCGTAACTGTAATCTGTAATCAGACCTGAGAGAGCAGCTTAACAGCTGACGAG 3000
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3001 GACAAAGCTGAAGCTCAACAAACAACTTCTAATCTGTAATCTGTAATCTGTAATCT 3060
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3061 GCGCGCAACGAGAGATTTGTAACATGCGAAGTGAAGTGAACATCTCGCGCGGAGATC 3120
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3121 ACGGAAACGAGATGCACTTACAGCCAGAAACAAACGATGAGGCTCTGAAAGCAAG 3180
3133 TGCACATGCTGAGAGACAGGTCATGATTTGAGGCGCTTAACGATGAGGCTGAGAG 3192
3181 TGCACATGCTGAGAGACAGGTCATGATTTGAGGCGCTTAACGATGAGGCTGAGAG 3240
3193 AAGAGCGCAGTGGAGGCGCTGAGAGAGCTGCTGAGTGAAGAAATCCCAAGTTTGA 3252

3241 AAGAGCGCAGTGGAGAGGCCCTGAGAGAGCTCTCGGAGTGAAGAAATCCCAAGTTTGA 3300
3253 TGTCCGTTTCGAGAGCTGACAGAAATGCTGACACCGAGAAAACAGACAGGCGAGAGCC 3312
3301 TGTCCGTTTCGAGAGCTGACAGAGATGCTGACACCGAGAAAACAGACAGGCGAGAGCC 3360
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3361 GATCAGCGGATCACGAGTCTCGCAGAGTGGAGAGCTGGGAGTGAAGAGCAAGGCT 3420
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3433 GACAGCTCAATGACCTGAGAGAAAGCATGCTATGCTTAAGTAATGCCGAAGCTTA 3492
3481 GACAGCTCAATGACCTGAGAGAAAGCATGCTATGCTTAAGTAATGCCGAAGCTTA 3540
3493 CAGCAGAGCTGAGAGCTGAACGAGAGCTCAAGAGAGGCTTCTGGAAGAGCAAGCCAA 3552
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3733 CAAACCAATCTATGATTTTCTGCAAGCCAAATGACCAACTGCTTAAGAAAAAG 3792
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3793 GGTTTATTTAGTCACGAGAAAGAGCCCTGCTTTAACCAACAGAGTCTCTGCAAGTAC 3852
3839 -----AGTTCTCTGCAAGTAC 3855
3853 AATGAGTGAAGCTGAGCCCTGAGAGAGAAAGCTGCTGAGAGCTGAGAGAGCC 3912
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4216 TGTCTGATACCGTGCATTTTGAACGCGAGGATCAATGCTGTAATGTCAGGTGAG 4275
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 Db 4336 ACACATTTACCCAGGCTTTTGGCGTGAACAAATGAATCTCCCAAGTCTCCAGACCAAG 4395
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 Db 4396 GAGCCAGCAGCAGCTTTGCACTGGAAGGGTGTATGAGGTGCGCCAGAAATACAAACGA 4455
 Qy 4453 GGAACAGCAAGGCTGGAGCAGGAAGTACATTTGCTTGAAGGATCAAAAGTCTCATTTAT 4512
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 Db 4576 GACGGGGATGTATCTATTGATGTCGCTTGTGCTTCCGAATCTCGAAATACAGGCCAA 4635
 Qy 4633 GCA----- 4635
 Db 4636 GCGATGTCCCATACATTAAGATGAATCTCACCCGACACACCTGTGCGCCGGG 4695
 Qy 4636 ----- 4635
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 Qy 4636 ----- 4662
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 Qy 4783 TTGAAAACTCCCTAATCCATGTCAGAGATTTGAGAGTCTTCCAAATTAATATATTC 4842
 Db 4936 TTGAAAACTCCCTAATCCATGTCAGAGATTTGAGAGTCTTCCAAATTAATATATTC 4995
 Qy 4843 AAGCACTGAGAGAGTACTCATGATAGCAGAGAGAGGGGCACTGTGTCTTGTGAC 4902
 Db 4996 AAGCACTGAGAGAGTACTCATGATAGCAGAGAGAGGGGCACTGTGTCTTGTGAC 5055
 Qy 4903 GTGAGAAAGTGAACAGTCCCTGCGCCAGTCCACCTGCTGCGCAGCCGACATCTCA 4962
 Db 5056 GTGAGAAAGTGAACAGTCCCTGCGCCAGTCCACCTGCTGCGCAGCCGACATCTCA 5115
 Qy 4963 CCCAATTTTGAAGCTGTCAAGGGGCTGCACTTTTGTGGGCAAGGCAAGATTGGAAC 5022
 Db 5116 CCCAATTTTGAAGCTGTCAAGGGGCTGCACTTTTGTGGGCAAGGCAAGATTGGAAC 5175
 Qy 5023 GGGCTCTGATCTGTGACAGCCTAGCCAGCAAAAGTGTCAATTTCTCGCTACAAAGAAAC 5082
 Db 5176 GGGCTCTGATCTGTGACAGCCTAGCCAGCAAAAGTGTCAATTTCTCGCTACAAAGAAAC 5235
 Qy 5083 CTCAGCAAAATCTGATCTCGGAAAGATAGAGACCTCAGAGCCTGACGCTGTATCCAC 5142
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Qy 5263 GCTCTTCAAGAGCTTCCCTGTCTCAATCGNAGAGGTGAACAGGCGAGGCGAGAG 5322
 Db 5416 GCTCTTCAAGAGCTTCCCTGTCTCAATCGNAGAGGTGAACAGGCGAGGCGAGAGAG 5475
 Qy 5323 GAGTACTTGTGTGTTCACCAAAATTTGAGGTGTGTGATTTCTTACCGAAAGCTTAC 5382
 Db 5476 GAGTACTTGTGTGTTCACCAAAATTTGAGGTGTGTGATTTCTTACCGAAAGCTTAC 5535
 Qy 5383 GCGACAGAGATCTCAAGTGAAGTGTGCTTACCTTTGGCTTTGCTTACAGAAACCTAT 5442
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 Qy 5623 AAGGAAACCTGTGAAGAGATCCGCACTGAACACACCGGGGCGCTTCCACCTCCGC 5682
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 Qy 5683 AG 5684
 Db 5836 AG 5837

RESULT 15
 US-10-791-666-3
 ; Sequence 3, Application US/10791666
 ; Publication No. US20040209297A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yu, Xuanhuan
 ; APPLICANT: Miranda, Maricar
 ; APPLICANT: Fridde, Carl Johan
 ; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
 ; FILE REFERENCE: LEX-0289-USA
 ; CURRENT APPLICATION NUMBER: US/10/791,666
 ; PRIOR FILING DATE: 2004-03-02
 ; PRIOR APPLICATION NUMBER: US/10/028,946
 ; PRIOR FILING DATE: 2001-12-20
 ; PRIOR APPLICATION NUMBER: US 60/258,335
 ; PRIOR FILING DATE: 2000-12-27
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 5877
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-10-791-666-3

Query Match 87.0%; Score 5358; DB 18; Length 5877;
 Best Local Similarity 95.8%; Pred. No. 0;
 Matches 5634; Conservative 0; Mismatches 5; Indels 243; Gaps 3;
 Qy 1 ATGTGAAGTTCAAAATATGAGCGCGGAATCTTTGATGCTGTGTGTAACCCATT 60
 Db 1 ATGTGAAGTTCAAAATATGAGCGCGGAATCTTTGATGCTGTGTGTAACCCATT 60
 Qy 61 GCGACCGCGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCAACCTTATGACTCA 120
 Db 61 GCGACCGCGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCAACCTTATGACTCA 120
 Qy 121 CAGCAGATGTCTCTCTTCTTCCGAGAGAGGATTAATGATGCCCTTTGTTCTTTGAA 180
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QY	181	GAATGCACTGACCTGCTCTGATGAAAGTAATGAACGAGCAACTTGTCCGGAGAT	240
Db	181	GAATGCACTGACCTGCTCTGATGAAAGTAATGAACGAGCAACTTGTCCGGAGAT	240
QY	241	TCCGACACCATAGCTGAGTTTACAGAGGTCACGCTTTCGCAAGACCTTGAAGTCA	300
Db	241	TCCGACACCATAGCTGAGTTTACAGAGGTCACGCTTTCGCAAGACCTTGAAGTCA	300
QY	301	AGCTTGTAGGTTGTGTCATCTTGTCTGAAGTGCAGGTGGTAAAGAGAAACCGGG	366
Db	301	AGCTTGTAGGTTGTGTCATCTTGTCTGAAGTGCAGGTGGTAAAGAGAAACCGGG	366
QY	361	GACATCTATGCTAAGAAAGTATGAAGAAGAGGCTTTATTTGGCCAGAGACGTTTCA	420
Db	361	GACATCTATGCTAAGAAAGTATGAAGAAGAGGCTTTATTTGGCCAGAGACGTTTCA	420
QY	421	TTTTTTGAGGAAGACGGAACATTTATTTCTCGAAGCAAGGCCGTTGATCCCAATT	480
Db	421	TTTTTTGAGGAAGACGGAACATTTATTTCTCGAAGCAAGGCCGTTGATCCCAATT	480
QY	481	CAGTATCCCTTTGAGCAAAAATACCTTTATCTGATGAGGAATATCAGCTGAGGG	540
Db	481	CAGTATCCCTTTGAGCAAAAATACCTTTATCTGATGAGGAATATCAGCTGAGGG	540
QY	541	GACTGTGTCACCTTTGAATTAATATGAGACACATTAATGAAACCTGATACGTTT	600
Db	541	GACTGTGTCACCTTTGAATTAATATGAGACACATTAATGAAACCTGATACGTTT	600
QY	601	TACCTAGCTGAGCTGATTTTGGCTGTTTCAAGCGTTCACTGATGAGGATACGTCATGA	660
Db	601	TACCTAGCTGAGCTGATTTTGGCTGTTTCAAGCGTTCACTGATGAGGATACGTCATGA	660
QY	661	GACATAGCGCTGAGAACATTTCTGCTTTCACCGCAACGATCAAGCTGTGATTTT	720
Db	661	GACATAGCGCTGAGAACATTTCTGCTTTCACCGCAACGATCAAGCTGTGATTTT	720
QY	721	GGATCTGCCGCGAAATGAAATTCAAACAGATGTAATGCCAACTCCCGATGGGACC	780
Db	721	GGATCTGCCGCGAAATGAAATTCAAACAGATGTAATGCCAACTCCCGATGGGACC	780
QY	781	CCAGATTAATAGGCTCTGAAGTCTGACTGTGATGAACGGGGATGAAAAAGCACTTAC	840
Db	781	CCAGATTAATAGGCTCTGAAGTCTGACTGTGATGAACGGGGATGAAAAAGCACTTAC	840
QY	841	GGCCTGGACTGTGACTGTGTCAGTGGGCGTGAATGCTATGAGATATTTAATGGAGA	900
Db	841	GGCCTGGACTGTGACTGTGTCAGTGGGCGTGAATGCTATGAGATATTTAATGGAGA	900
QY	901	TCCCCCTTGCAGAGGGAACTTCTGCAGAACCTTCAATTAATTATGAATTTCAAGGAG	960
Db	901	TCCCCCTTGCAGAGGGAACTTCTGCAGAACCTTCAATTAATTATGAATTTCAAGGAG	960
QY	961	TTTTTGAATTTCCAGATGAACCCCAAGAGGACATGACTTCTTGATCTGATCAANGC	1020
Db	961	TTTTTGAATTTCCAGATGAACCCCAAGAGGACATGACTTCTTGATCTGATCAANGC	1020
QY	1021	TTGTTGTGCGCCAGAAAAGAGACTGAAGTTTGAAGGCTTTTGTGCTGCATCCCTTTC	1080
Db	1021	TTGTTGTGCGCCAGAAAAGAGACTGAAGTTTGAAGGCTTTTGTGCTGCATCCCTTTC	1080
QY	1081	TCTAAATATGACTGGAACAACATTGTGTACTCTCTCCCTCTGTCCACCCCTCAAG	1140
Db	1081	TCTAAATATGACTGGAACAACATTGTGTACTCTCTCCCTCTGTCCACCCCTCAAG	1140
QY	1141	TCTGACATGACACCTCCATTTTGAATGAACAGAGAAATTTGGGCTTTCATCCCTCT	1200
Db	1141	TCTGACATGACACCTCCATTTTGAATGAACAGAGAAATTTGGGCTTTCATCCCTCT	1200
QY	1201	CCGTCGCACTGAGCCCTCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCG	1260
Db	1201	CCGTCGCACTGAGCCCTCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCG	1260

QY	1261	TACGAGAACGCACTGGAGATTCTTGGAATCTGACTCTGTGTGTGGGATCTGACTCC	132
Db	1261	TACGAGAACGCACTGGAGATTCTTGGAATCTGAATCTGTGTGTGGGATCTGACTCC	132
QY	1321	CTGCGCAAGCTAGCTCATGTGAAAAAACTTCTCATMAAAGCAAAAGCTACAGAC	138
Db	1321	CTGCGCAAGCTAGCTCATGTGAAAAAACTTCTCATMAAAGCAAAAGCTACAGAC	138
QY	1381	TTCTCAGACCAAGTGTCACAAGATGAGCAGAAATGACCCGGTTACATCGAGAGTGTCA	144
Db	1381	TTCTCAGACCAAGTGTCACAAGATGAGCAGAAATGACCCGGTTACATCGAGAGTGTCA	144
QY	1441	GAGGTGAGGCTGTGCTTAGTACAGAGGAGGTGAGCTGAAGGCTTGAAGCTACAGAC	150
Db	1441	GAGGTGAGGCTGTGCTTAGTACAGAGGAGGTGAGCTGAAGGCTTGAAGCTACAGAC	150
QY	1501	TCCTCTCTGAGCAGGACCTTGCTACATCAAGATGACGTATGCTTAAAGCGAAGT	156
Db	1501	TCCTCTCTGAGCAGGACCTTGCTACATCAAGATGACGTATGCTTAAAGCGAAGT	156
QY	1561	TTGGAGCAAGCAACGATGAGGTGTCCTCCAGAGAGTGAACAAGCACTGACGTTCCAT	1620
Db	1561	TTGGAGCAAGCAACGATGAGGTGTCCTCCAGAGAGTGAACAAGCACTGACGTTCCAT	1620
QY	1621	GATATCAGAGACAGAGCCGAGAGCTCCAAAGAAATCAAGAGCAGAGATCAACAGGCTCA	1680
Db	1621	GATATCAGAGACAGAGCCGAGAGCTCCAAAGAAATCAAGAGCAGAGATCAACAGGCTCA	1680
QY	1681	GTGGAAGAAATAGAGTTGATGATGATAGTTGAGAGAGATCTTGTCTCAGCAAGAGA	1740
Db	1681	GTGGAAGAAATAGAGTTGATGATGATAGTTGAGAGAGATCTTGTCTCAGCAAGAGA	1740
QY	1741	CGAGATGATCTCTAGAACTGAGCTGAGAGAGTCTGGGCTTGTGCTGAGAAATTCAG	1800
Db	1741	CGAGATGATCTCTAGAACTGAGAGTCTGAGAGAGTCTGGGCTTGTGCTGAGAAATTCAG	1800
QY	1801	CGGAAAGCGACAGAAATGTACAGATMAACTGTTGAAGCTAAGATCAAGGAGACCTGAA	1860
Db	1801	CGGAAAGCGACAGAAATGTACAGATMAACTGTTGAAGCTAAGATCAAGGAGACCTGAA	1860
QY	1861	GTGGAGAAATTTGGGAACTGGAGAAAGATCAATCTGACAGAGCTCAAAATTCAGAG	1920
Db	1861	GTGGAGAAATTTGGGAACTGGAGAAAGATCAATCTGACAGAGCTCAAAATTCAGAG	1920
QY	1921	CTCCAAAGAAACTGGAGAGGCT-----	1944
Db	1921	CTCCAAAGAAACTGGAGAGGCTGTATAAAGCCAGACCGAGGCTCAACCGAGCTGTGAG	1980
QY	1945	-----GGAAGAGGCGAGCCGAGAGGAGGCTGGAGAAAGCTGCAAAACCGAGAG	1992
Db	1961	AATATCCGCGCAGGCGAAAGAGCGAGCCGAGAGGAGCTGGAGAAAGCTGCAAAACCGAGAG	2040
QY	1993	GATTCTTCTGAGGCATCAGAAAGAACTGATGAGAGCTGAGGAAAGCGCGCAATTCCTG	2052
Db	2041	GATTCTTCTGAGGCATCAGAAAGAACTGATGAGAGCTGAGGAAAGCGCGCAATTCCTG	2100
QY	2053	GAGAAACAAGTTAAAGAGACTAGAGACCTAGAGCCTTAGAGAAACAAGCTGAAGATGAC	2112
Db	2101	GAGAAACAAGTTAAAGAGACTAGAGACCTAGAGCCTTAGAGAAACAAGCTGAAGATGAC	2160
QY	2113	ATCCAGACAATAATCCCAACAGATCCACAGACATGAGCTGATTAATTTCTGAGCTTCAGAG	2172
Db	2161	ATCCAGACAATAATCCCAACAGATCCACAGACATGAGCTGATTAATTTCTGAGCTTCAGAG	2220
QY	2173	AAACATGGGAGGCCCAAGTCTCAGCCACAGCACTTAGAGTGCACTGAAACAGAAAG	2232
Db	2221	AAACATGGGAGGCCCAAGTCTCAGCCACAGCACTTAGAGTGCACTGAAACAGAAAG	2280
QY	2233	CAGACATATAGAGAAAGATTAATAGTTGTGACAAATCAATTAAGAAAGCTGGCTGAC	2292
Db	2281	CAGACATATAGAGAAAGATTAATAGTTGTGACAAATCAATTAAGAAAGCTGGCTGAC	2340
QY	2293	AAGAGACACTGAGAACATGATGCGAGACACAGAGAGAGGCGCATGAGAAAGGCAAA	2352

Db 2341 AAGAGACACTGGAGAACATGATGACAGACACGAGAGAGGCGCATGAGAAAGGCGAA 2400
Qy 2353 ATTCTCAGCGAACAAGAGCGATGATCAATGCTTAGATTCAGATCAGATCCCTGGA 2412
Db 2401 ATTCTCAGCGAACAAGAGCGATGATCAATGCTTAGATTCAGATCAGATCCCTGGA 2460
Qy 2413 CAGAGATTGTGGAATGCTGTGAAGCCATTAACTTGACCAATAGCAGTCTTTTACC 2472
Db 2461 CAGAGATTGTGGAATGCTGTGAAGCCATTAACTTGACCAATAGCAGTCTTTTACC 2520
Qy 2473 CAAAGGACATGAGGCGCAAGAGATGATTTCTGAATCTCAGGCAACGAAATTTAC 2532
Db 2521 CAAAGGACATGAGGCGCAAGAGATGATTTCTGAATCTCAGGCAACGAAATTTAC 2580
Qy 2533 CTGGAGACA CAGGCTGGGAAGTTGAGGCCAGAACCGAAACTGAGAGACGCTGAG 2592
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Qy 2593 AAGATCAGCA CCAAGACCAAGTGA CAAAGATCGGCTGCTGGAATCTGAGACAAATG 2652
Db 2641 AAGATCAGCA CCAAGACCAAGTGA CAAAGATCGGCTGCTGGAATCTGAGACAAATG 2700
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Db 2701 CCGGAGGTCA GTTAGAGACAGAGAGCAGAACTGAGCTCAAGCGCAGCTCAGAG 2760
Qy 2713 CTACAGCTCTCCCTGAGAGCGCGAGTCA CAGTTGACAGCCCTGAGGCTGACGAG 2772
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Qy 2773 GCCCTGAGAGCCAGCTTGGCCAGGGAAGACAGACTGGAAGACACACAGAAAGCT 2832
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Qy 2833 GAAGAGAGATCCAGGCACTCAGGCACTAGAGATGAATCCAGGCGCAATTTGATGCT 2892
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Db 4861 AAGACCTGAGAAAGCTACTCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4920
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Db 4921 GTGAAGAAAGTAAACAGTCCCTGTGACCACTGCTGCTGCTGCTGCTGCTGCTG 4980
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Qy 5041 GGGCTGTGATCTGTGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5100
Db 5041 GGGCTGTGATCTGTGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5100
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Db 5281 GCTCTTCACAGCTCCCTGTCTCAATCGGAGGTGAGACAGGAGAGAGAGAGAGAG 5340
Qy 5341 GAGTACTGTGTGTGTTCCAGAAATTTGAGAGTGTGATGATTTCTTACGAAAGAGTAC 5400
Db 5341 GAGTACTGTGTGTGTTCCAGAAATTTGAGAGTGTGATGATTTCTTACGAAAGAGTAC 5400
Qy 5401 CGCAGAGAGATCTGAGAGTGTGAGTGTGATGATTTCTTACGAAAGAGTAC 5460
Db 5401 CGCAGAGAGATCTGAGAGTGTGAGTGTGATGATTTCTTACGAAAGAGTAC 5460
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Db 5461 CTGTTTGTGACCACTTCACTCATCGAAGTAAATGATTCAGAGGAGAGGCTCCAGCA 5520
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Db 5521 GGGAGCCCTGCGCGAGCTTACCTGAGCATCCGAAACCGGCTACTGAGGCTGCTGCTG 5580
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Db 5581 TCCCTAGAGAGATTTATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5640

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Db 5641 AAGGAAACCTGTGTAAGAGAGTCCGACATGAAACACACCGGGGCGCCGCTCCAGC 5700
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Db 5761 TCCAGCCAGAGGCGCGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5820
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Db 5821 TACCGAGAGAGGCGAG 5880
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Qy 5941 GAG 6000
Db 5941 GAG 6000
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Qy 6181 GCAAGATTCATGATCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6240
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Qy 6361 GAG 6420
Db 6361 GAG 6420
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Db 6421 TAGCAG 6480
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RESULT 2
US-10-325-430-10
; Sequence 10, Application US/10325430
; Publication No. US2003015325A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc

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APPLICANT: Siles-Santiago, Immaculada
APPLICANT: Rosenfeld, Julie Beth
TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
FILE REFERENCE: 32838, 336 and 52908
CURRENT APPLICATION NUMBER: US/10/325,430
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US 60/341,953
PRIOR FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 6574
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-325-430-10

Query Match      100.0%; Score 6574; DB 16; Length 6574;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6574; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1 AGAGCCGCGAGTGGGGAGATGTTGAAATTAATATGAGCGCGAATCCTTGTGATGCT 60
QY      61 GGTGCTGCTGAACCCATTGCGACCGGGCTCCAGGCTGATTTGTTTCCAGGGGAAA 120
DB      61 GGTGCTGCTGAACCCATTGCGACCGGGCTCCAGGCTGATTTGTTTCCAGGGGAAA 120
QY      121 CCAACCTTTATGACTCAAGCAGAGATGTCCTCTTCCGAGAGAGATATTAGATGCC 180
DB      121 CCAACCTTTATGACTCAAGCAGAGATGTCCTCTTCCGAGAGAGATATTAGATGCC 180
QY      181 CTCTTGTCTCTTTGAGAAATGCACTGACCTGCTCTGATGAAATTAAGACGTGAC 240
DB      181 CTCTTGTCTCTTTGAGAAATGCACTGACCTGCTCTGATGAAATTAAGACGTGAC 240
QY      241 AACTTGTCCGGAAGTATCCGACACATATGCTGATTAAGAGCTCCAGCTTTGGCA 300
DB      241 AACTTGTCCGGAAGTATCCGACACATATGCTGATTAAGAGCTCCAGCTTTGGCA 300
QY      301 AAGGACTTGAAGTCAAGAGCTGTGAGGTGTCCTGCTGATGAGAGAGAGTGA 360
DB      301 AAGGACTTGAAGTCAAGAGCTGTGAGGTGTCCTGCTGATGAGAGAGAGTGA 360
QY      361 AAGAGAAAGCAACCGGGACATCTATGCTATGAAAGTGAAGAAAGGCTTTATTG 420
DB      361 AAGAGAAAGCAACCGGGACATCTATGCTATGAAAGTGAAGAAAGGCTTTATTG 420
QY      421 GCCCAGAGCAGGTTCAATTTTGAAGAAAGCGGAAACATATTATCTGGAAGCAAGC 480
DB      421 GCCCAGAGCAGGTTCAATTTTGAAGAAAGCGGAAACATATTATCTGGAAGCAAGC 480
QY      481 CCGTGATCCCAATTAAGATGCTTTCAAGAGCAAAATCACTTTATCTGATGAG 540
DB      481 CCGTGATCCCAATTAAGATGCTTTCAAGAGCAAAATCACTTTATCTGATGAG 540
QY      541 GAATATCAGCTGAGAGGAGCTTGCTGCACTTTTGAATATGATATGAGACAGTTAGAT 600
DB      541 GAATATCAGCTGAGAGGAGCTTGCTGCACTTTTGAATATGATATGAGACAGTTAGAT 600
QY      601 GAAAACCTGATACGTTTAACTAGCTGAGCTGATTTGGCTGTTCAAGCTTCACTG 660
DB      601 GAAAACCTGATACGTTTAACTAGCTGAGCTGATTTGGCTGTTCAAGCTTCACTG 660
QY      661 ATGGGATAGTGATGAGACATCAAGCTGAGACATTTCTGTTGACCGACAGAGAC 720
DB      661 ATGGGATAGTGATGAGACATCAAGCTGAGACATTTCTGTTGACCGACAGAGAC 720
QY      721 ATCAAGCTGTGATTTTGGATCTGCGGAAATGAAATTCAAACAAGATGTGAATGCC 780
DB      721 ATCAAGCTGTGATTTTGGATCTGCGGAAATGAAATTCAAACAAGATGTGAATGCC 780
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DB      781 AAATCCCGATTGGAGCCCGAGATTACATGCTCCTGAAGTGTGACTGATGAAACGGG 840
QY      841 GATGAAAAGGACCTACGAGCTGAGCTGATGATGATGATGATGATGATGATGATGAT 900
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QY      901 GAGATGATTTATGAGAGATCCCTTCCGAGAGGAACTTCCGAGAACTTCAATAC 960
DB      901 GAGATGATTTATGAGAGATCCCTTCCGAGAGGAACTTCCGAGAACTTCAATAC 960
QY      961 ATTATGATTTCCAGAGGTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTGA 1020
DB      961 ATTATGATTTCCAGAGGTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTGA 1020
QY      1021 CTGATCTGATTCAAAGCTTGTGTCGCGCCAGAAAGAGAGACTGAAGTTGAAGTCTT 1080
DB      1021 CTGATCTGATTCAAAGCTTGTGTCGCGCCAGAAAGAGAGACTGAAGTTGAAGTCTT 1080
QY      1081 TGTGCTCATCTTTCTTCTTAAATTTGACTGGAACACATTGTAATCTCTCCCTCC 1140
DB      1081 TGTGCTCATCTTTCTTCTTAAATTTGACTGGAACACATTGTAATCTCTCCCTCC 1140
QY      1141 TTGCTTCCAGCCCTCAAGCTGAGATGACACCTCCAAATTTGATGAACAGAGAAAT 1200
DB      1141 TTGCTTCCAGCCCTCAAGCTGAGATGACACCTCCAAATTTGATGAACAGAGAAAT 1200
QY      1201 TGTGAGGTTCAATCTCTCTGTCGAGAGTGAAGCTTCTGAGGTTGAGAAACTG 1260
DB      1201 TGTGAGGTTCAATCTCTCTGTCGAGAGTGAAGCTTCTGAGGTTGAGAAACTG 1260
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DB      1261 CCGTTTGTGGGTTTTCGTAAGCAAGGCACTGGGATTTCTGATGATGATGATGAT 1320
QY      1321 GGTGAGGCTGAGACCTCCCTGCAAGACTAGCTCATGAAAGAACTTCTCATCAAA 1380
DB      1321 GGTGAGGCTGAGACCTCCCTGCAAGACTAGCTCATGAAAGAACTTCTCATCAAA 1380
QY      1381 AGCAAAAGACTCAAGACTCTGAGCAAGTGTCAAGATGAGAGAGAAATGACCCGG 1440
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QY      1441 TTACATCGAGAGTGTCAAGAGTGAAGGCTGTGCTTAATCAGAGAGAGTGAAGT 1500
DB      1441 TTACATCGAGAGTGTCAAGAGTGAAGGCTGTGCTTAATCAGAGAGAGTGAAGT 1500
QY      1501 GCTCTGAGACTCAAGATCCCTCTGAGAGAGAGCTTGTCAATCAACAGATATC 1560
DB      1501 GCTCTGAGACTCAAGATCCCTCTGAGAGAGAGCTTGTCAATCAACAGATATC 1560
QY      1561 AGTAGCTTAAACGAATTTGAGAGCAAGCAGATGAGAGTGTCCAGAGAGATGACAA 1620
DB      1561 AGTAGCTTAAACGAATTTGAGAGCAAGCAGATGAGAGTGTCCAGAGAGATGACAA 1620
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DB      1621 GCACTGACACTTCTCATATATCAGAGAGCAGAGCCGGAACCTCAAAATTCAGAG 1680
QY      1681 CAGAGTACCAAGCTCAAGTGAAGAAATGAGTGAATGAATAGTGAAGAGAT 1740
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QY      1741 CTGTGCTCAGCAAGAGAGAGATCTCTAGATCTGAGCTGAGAGAGTCTGGCTT 1800
DB      1741 CTGTGCTCAGCAAGAGAGAGATCTCTAGATCTGAGCTGAGAGAGTCTGGCTT 1800
QY      1801 GCTGCTGAAGAAATTCAGCGGAAAGGACAGAAATGACATTAACCTGTTGAAGCTTA 1860
DB      1801 GCTGCTGAAGAAATTCAGCGGAAAGGACAGAAATGACATTAACCTGTTGAAGCTTA 1860
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QY 1861 GATCAAGGAGAGCTGGAAGTGGAGATATGCGAAA CTGGAGAGATCAATGCTGGAGC 1920
DB 1861 GATCAAGGAGAGCTGGAAGTGGAGATATGCGAAA CTGGAGAGATCAATGCTGGAGC 1920
QY 1921 CAGCTCAAAATTCAGAGAGCTCCAAAGAAA CTGAGAGAGCTGCAAAAGAGCGAGCCGAG 1980
DB 1921 CAGCTCAAAATTCAGAGAGCTCCAAAGAAA CTGAGAGAGCTGCAAAAGAGCGAGCCGAG 1980
QY 1981 AGGAGAGCTGGAGAGAGCTGCAAGAACCGAGAGAGATCTTCTTGAAGGATCAAGAAAGAGCTG 2040
DB 1981 AGGAGAGCTGGAGAGAGCTGCAAGAACCGAGAGAGATCTTCTTGAAGGATCAAGAAAGAGCTG 2040
QY 2041 GTGGAGAGCTGAGAGAGAGCGCCGCAATCTCTGGAGAGCAAGGTAAAGAGACTGAGAGACCATG 2100
DB 2041 GTGGAGAGCTGAGAGAGAGCGCCGCAATCTCTGGAGAGCAAGGTAAAGAGACTGAGAGACCATG 2100
QY 2101 GAGCGTAGAGAAAACAGACTGAAAGATGACATCCAGACAAAATCCCAAGATCCAGAGC 2160
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DB 3841 GCTTTACCAACACAGTTTCCCTGCAATCAATGAGCTGAAGCTG GCGCTGAGAGAGAG 3900
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DB 3961 GCCCGGAGAGAGAGTGGCCACCGCAAGCAACCGAACCAACCAT CCAAGCCAGCC 4020
QY 4021 ACCGAGAGCAGAGATCGCATGCTCGGCAATCGTGGCTGCGCAGAG CAGACCGCAGT 4080

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Qy	4081	GCATAGAGCTCTGTGGCCCCCGGCATCCAGCCGACAGAAAGAGTCTTCAATTCACAGAGAA	4140
Dp	4081	GGCATGAGACCTGTGCTGGCCCCCGGCATCCAGCCGACAGAAAGAGTCTTCAATTCACAGAGAA	4140
Qy	4141	TTTACTCGGCGCTTTAAGGAAGCATGCAACCAATATTCTCAACCAATTCAGTAA	4200
Dp	4141	TTTACTCGGCGCTTTAAGGAAGCATGCAACCAATATTCTCAACCAATTCAGTAA	4200
Qy	4201	CTGAACATGCGAGCCACAAAGTGTCTGTGTCTGAAATACCGTSCATCTTTGGACGCGAG	4266
Dp	4201	CTGAACATGCGAGCCACAAAGTGTCTGTGTCTGAAATACCGTSCATCTTTGGACGCGAG	4266
Qy	4261	GCATCCAAATGCTTCGAAATGTCAGGTGATGTGTCAACCCAAAGTGTCTCCACGTCTTGCCA	4320
Dp	4261	GCATCCAAATGCTTCGAAATGTCAGGTGATGTGTCAACCCAAAGTGTCTCCACGTCTTGCCA	4320
Qy	4321	GCCACTCTGCGGCTCTGCTGTGAATATGCAACATTCACCGAAGCTTTCTGCCGTGAC	4380
Dp	4321	GCCACTCTGCGGCTCTGCTGTGAATATGCAACATTCACCGAAGCTTTCTGCCGTGAC	4380
Qy	4381	AAAATGAACCTCCCGACGATCTCCAGACCAAAGAGCCACACAGCTGTCCACGTCTTGCCA	4440
Dp	4381	AAAATGAACCTCCCGACGATCTCCAGACCAAAGAGCCACACAGCTGTCCACGTCTTGCCA	4440
Qy	4441	TGATGAAGGTGCCCCAGGATATACAAACGAGGACAGCAAGCTGGACAGGAATACATT	4500
Dp	4441	TGATGAAGGTGCCCCAGGATATACAAACGAGGACAGCAAGCTGGACAGGAATACATT	4500
Qy	4501	GTCTCTGGAGGGAATCAAAAGTCTCTCATTTATGACAAATGAAGCCAGAGAACTGACACAGG	4560
Dp	4501	GTCTCTGGAGGGAATCAAAAGTCTCTCATTTATGACAAATGAAGCCAGAGAACTGACACAGG	4560
Qy	4561	CCGGTGAAGAAATTTGAAGCTGTGCTTCCGACCGGGAGTGAATCATTCATGATGGCCGTT	4620
Dp	4561	CCGGTGAAGAAATTTGAAGCTGTGCTTCCGACCGGGAGTGAATCATTCATGATGGCCGTT	4620
Qy	4621	GGTGCTTCCGAATCTCGCAAAATACAGCCAAACAGAAAGCAGAAAGCTGATGCTAAACTG	4680
Dp	4621	GGTGCTTCCGAATCTCGCAAAATACAGCCAAACAGAAAGCAGAAAGCTGATGCTAAACTG	4680
Qy	4681	CTTGGAATCTCCCTGTGCTGAAACTGGAGAGTATGACCGTCTTACATGAACTGCACGCTG	4740
Dp	4681	CTTGGAATCTCCCTGTGCTGAAACTGGAGAGTATGACCGTCTTACATGAACTGCACGCTG	4740
Qy	4741	CCCTTCAAGTACCAAGTGTGTGTGTGGGACCCAGAGAAAGGGCTCTACGCCCTTAATGTC	4800
Dp	4741	CCCTTCAAGTACCAAGTGTGTGTGTGGGACCCAGAGAAAGGGCTCTACGCCCTTAATGTC	4800
Qy	4801	TTGAAGAACTCCCTTAAACCATGTGCCAGAGAAATTTGAGACAGTCTTCCAAATTTATATTATC	4860
Dp	4801	TTGAAGAACTCCCTTAAACCATGTGCCAGAGAAATTTGAGACAGTCTTCCAAATTTATATTATC	4860
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Dp	4861	AAGACCTGAGAAAGCTACTCATGATATGACAGAGAAAGGCGGACATGTGTCTTGTGGAC	4920
Qy	4921	GTGAAGAAAGTGAACAGTCTCCCTGGCCACAGTCCACCTGTCCAGCCGACATCTCA	4980
Dp	4921	GTGAAGAAAGTGAACAGTCTCCCTGGCCACAGTCCACCTGTCCAGCCGACATCTCA	4980
Qy	4981	CCCAACATTTTGAAGCTGTCAAGGGGCTGCACCTGTTTGGGGGACAGCAATTGAAGAC	5040
Dp	4981	CCCAACATTTTGAAGCTGTGTCAAGGGGCTGCACCTGTTTGGGGGACAGCAATTGAAGAC	5040
Qy	5041	GGGCTCTGCACTGTGCAAGCCATGCCACAGCAAGTGTCTTCTCCGCTACAGAAAC	5100
Dp	5041	GGGCTCTGCACTGTGCAAGCCATGCCACAGCAAGTGTCTTCTCCGCTACAGAAAC	5100
Qy	5101	CTCAGCAAAATCTGCTATCCGGAAGAGATAGAGCTTCAGAGCCCTGACGTATATCAC	5160
Dp	5101	CTCAGCAAAATCTGCTATCCGGAAGAGATAGAGCTTCAGAGCCCTGACGTATATCAC	5160

QY	5161	TTCAACCAATTACAGATATCTCATTTGGAACCAATAAATCTACGAAATGACATGAAGAC	5222
Db	5161	TTCAACCAATTACAGATATCTCATTTGGAACCAATAAATCTACGAAATGACATGAAGAC	5222
QY	5221	TACACGCTCGAGGAATTCCTGGATAGAAATGACAAATTCCTTGGCACCTGTGTGTTGCC	5280
Db	5221	TACACGCTCGAGGAATTCCTGGATAGAAATGACAAATTCCTTGGCACCTGTGTGTTGCC	5280
QY	5281	GCCCTTTCGCAACAGTTTCCCTGTCTCAATCGTGCAGGTGAAACGCGCAGGGCAGCGAAG	5340
Db	5281	GCCCTTTCGCAACAGTTTCCCTGTCTCAATCGTGCAGGTGAAACGCGCAGGGCAGCGAAG	5340
QY	5341	GAGTACTTGTGTGTGTTCCAGAAATTTGGAATGTTCGGATGTTCTTACGGAAGACGTAGC	5400
Db	5341	GAGTACTTGTGTGTGTTCCAGAAATTTGGAATGTTCGGATGTTCTTACGGAAGACGTAGC	5400
QY	5401	CGCACAGACGATCTCAAGTGGAGTCCGCTTACCTTTGGCTTTGCGCTACAGAAACCTTAT	5460
Db	5401	CGCACAGACGATCTCAAGTGGAGTCCGCTTACCTTTGGCTTTGCGCTACAGAAACCTTAT	5460
QY	5461	CTGTTTGGACCGCACTTCACTCACTGAAATTAAGATCCAGGACCGCTCCACGCA	5520
Db	5461	CTGTTTGGACCGCACTTCACTCACTGAAATTAAGATCCAGGACCGCTCCACGCA	5520
QY	5521	GCGACCCCTGCGCAGCGTACCTGACATCCCGAACCGCGCTACCTGGGCGCTGCATT	5580
Db	5521	GCGACCCCTGCGCAGCGTACCTGACATCCCGAACCGCGCTACCTGGGCGCTGCATT	5580
QY	5581	TCCTTCAGAGAGGATTTACTTGGCGTCTCTCATACAGATTAATTAAGGCTCATTTGCTGC	5640
Db	5581	TCCTTCAGAGAGGATTTACTTGGCGTCTCTCATACAGATTAATTAAGGCTCATTTGCTGC	5640
QY	5641	AAGGAAACCTCGTGAAGAGATCCGGCACGTAAACCAACCGGGGCGGTCACCTCCGCG	5700
Db	5641	AAGGAAACCTCGTGAAGAGATCCGGCACGTAAACCAACCGGGGCGGTCACCTCCGCG	5700
QY	5701	AGCACCCCCCAACAGCAGAGGCCCAACCCACGTTACACAGACATACCAAGCGGCTGGCC	5760
Db	5701	AGCACCCCCCAACAGCAGAGGCCCAACCCACGTTACACAGACATACCAAGCGGCTGGCC	5760
QY	5761	TCCAGGCCAGGGCGCGCGCGAAGGGCCGAGCCACCGGGAGAGGCCAACAACCCCAACGCG	5820
Db	5761	TCCAGGCCAGGGCGCGCGCGAAGGGCCGAGCCACCGGGAGAGGCCAACAACCCCAACGCG	5820
QY	5821	TACCGCAGAGGGCGCGACCCGACCTGCGAGGAGCAAGTCTCTGCGCGCCCTCTGAGAGCA	5880
Db	5821	TACCGCAGAGGGCGCGACCCGACCTGCGAGGAGCAAGTCTCTGCGCGCCCTCTGAGAGCA	5880
QY	5881	GAGAAATTCCTCCGGCCGATGCTCAGCAACGCGGAGAGACGCGTCCCGCGGAGGCTGTTT	5940
Db	5881	GAGAAATTCCTCCGGCCGATGCTCAGCAACGCGGAGAGACGCGTCCCGCGGAGGCTGTTT	5940
QY	5941	GAAAGACAGCAGCAGAGGGCCGCGCTGCGCGGGAGACCGTNGAGAACCCCGCGTCCCAAGTG	6000
Db	5941	GAAAGACAGCAGCAGAGGGCCGCGCTGCGCGGGAGACCGTNGAGAACCCCGCGTCCCAAGTG	6000
QY	6001	AACAAAGGAAAGGGCAGAGTGCTCTCAAGTTTTCACGCTTAACTGTCACTTAT	6060
Db	6001	AACAAAGGAAAGGGCAGAGTGCTCTCAAGTTTTCACGCTTAACTGTCACTTAT	6060
QY	6061	GACTGGAATTAAGAGCTGTCACACCTGCAAGCTTAACTGCTCAGTCCGAGGATCATCCAG	6120
Db	6061	GACTGGAATTAAGAGCTGTCACACCTGCAAGCTTAACTGCTCAGTCCGAGGATCATCCAG	6120
QY	6121	CTGATGAGAGAAATCCCGCAGCAGGTGAAAGCTGTTCTGAGAACAGATTATTCGTGA	6180
Db	6121	CTGATGAGAGAAATCCCGCAGCAGGTGAAAGCTGTTCTGAGAACAGATTATTCGTGA	6180
QY	6181	GCAAGATTCAATGTGACTCTTACAGACGTGTGACTTTAAAAATGCGCTTAAAGCTGCAGAGC	6240
Db	6181	GCAAGATTCAATGTGACTCTTACAGACGTGTGACTTTAAAAATGCGCTTAAAGCTGCAGAGC	6240

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QY 6241 CAGCCACCTCTGCTTACAAAAAGAGTACTTAGTGCACATGACTGTAAAGAAACATTGTAA 6300
Db 6241 CAGCCACCTCTGCTTACAAAAAGAGTACTTAGTGCACATGACTGTAAAGAAACATTGTAA 6300
QY 6301 AACCCATCTAGAAATTCAGAAAGCTCTTAATTCTTATAGAAATGACACCTCCCTGGAGCC 6360
Db 6301 AACCTCATCTAGAAATTCAGAAAGCTCTTAATTCTTATAGAAATGACACCTCCCTGGAGCC 6360
QY 6361 GAGAGACATCTGTTGTTGATTTTGAAGGACAGGACAGCAACCACTGTATTTAGTTCCA 6420
Db 6361 GAGAGACATCTGTTGTTGATTTTGAAGGACAGGACAGCAACCACTGTATTTAGTTCCA 6420
QY 6421 TAGCCAGGCTTAAACAGGACCAAGTGGCTGGCTTTAAAAACACACAGATGACTGGAAATG 6480
Db 6421 TAGCCAGGCTTAAACAGGACCAAGTGGCTGGCTTTAAAAACACACAGATGACTGGAAATG 6480
QY 6481 ATGTGTGGCTCAGTCCCTGTTTCCAGAAATTTTACGTGCAAGAGATTAGATTCATTT 6540
Db 6481 ATGTGTGGCTCAGTCCCTGTTTCCAGAAATTTTACGTGCAAGAGATTAGATTCATTT 6540
QY 6541 TTGGCTTAAGAAAAATCGAAGATGTAGTTTGA 6574
Db 6541 TTGGCTTAAGAAAAATCGAAGATGTAGTTTGA 6574

RESULT 3
US-10-757-262-51
; Sequence 51, Application US/10757262
; Publication No. US20040197825A1
GENERAL INFORMATION:
APPLICANT: Karicheti, Venkateswarlu
APPLICANT: Silos-Santiago, Immaculada
APPLICANT: Eliasof, Scott D.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
TITLE OF INVENTION: 15340, 11852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
TITLE OF INVENTION: 85017, 155, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84280, 2882, 8203, 32678 OR
TITLE OF INVENTION: 55053
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CURRENT APPLICATION NUMBER: US/10757,262
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PRIOR FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: US 60/457,901
PRIOR FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: US 60/468,775
PRIOR FILING DATE: 2003-05-08
PRIOR APPLICATION NUMBER: US 60/471,614
PRIOR FILING DATE: 2003-05-19
PRIOR APPLICATION NUMBER: US 60/478,742
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: US 60/488,529
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/491,156
PRIOR FILING DATE: 2003-07-30
PRIOR APPLICATION NUMBER: US 60/499,594
PRIOR FILING DATE: 2003-09-02
PRIOR APPLICATION NUMBER: US 60/506,332
PRIOR FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 136
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 51
LENGTH: 6574
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:

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Query Match	Best Local Similarity	Conservative	Mismatches	Indels	Gaps
100.0%; Score 6574; DB 18; Length 6574;	100.0%; Pred. No. 0;	0;	0;	0;	0;
Matches 6574;					
NAME/KEY: CDS					
LOCATION: (119) ... (6180)					
US-10-757-262-51					
1	AGAGCCGCACTGGGAGATGTTGAAGTTCAATATATGAGGCGGAAATCCTTTGGATGCT	60			
1	AGAGCCGCACTGGGAGATGTTGAAGTTCAATATATGAGGCGGAAATCCTTTGGATGCT	60			
61	GATGTCGTGAACCATTTGCCAGCGCGGCGCTCCAGGCTGAAATCTGTTCTTCCAGGGGAAA	120			
61	GATGTCGTGAACCATTTGCCAGCGCGGCGCTCCAGGCTGAAATCTGTTCTTCCAGGGGAAA	120			
121	CCACCCCTTATGACTCAACAGCAGATGCTCTCTTCCGAGAAAGGATATATGATGCC	180			
121	CCACCCCTTATGACTCAACAGCAGATGCTCTCTTCCGAGAAAGGATATATGATGCC	180			
181	CTCTTTGTTCTTTGAAAGATGCAAGTCAGCTGCTCTGATGAAGATTAGCAGTGAAC	240			
181	CTCTTTGTTCTTTGAAAGATGCAAGTCAGCTGCTCTGATGAAGATTAGCAGTGAAC	240			
241	AACTTTGTCGGGAAGTATCCGACACCATACCTAGATGATGACAGGCTTCAGGCTCCGCA	300			
241	AACTTTGTCGGGAAGTATCCGACACCATACCTAGATGATGACAGGCTTCAGGCTCCGCA	300			
301	AAGACTTCGAAGTCAGAAAGTCTTGAGGTTGTGATCACTTTGCTGAAGTGCAGTGGTA	360			
301	AAGACTTCGAAGTCAGAAAGTCTTGAGGTTGTGATCACTTTGCTGAAGTGCAGTGGTA	360			
361	AGAGGAAAGCAACCGGGGACATCTATGCTATGAAAGTATGAAGAAAGGCTTTATG	420			
361	AGAGGAAAGCAACCGGGGACATCTATGCTATGAAAGTATGAAGAAAGGCTTTATG	420			
421	GCCGAGAGAGAGGTTCAATTTTGAAGAAAGGGAACATATATCTCGAAGACAGC	480			
421	GCCGAGAGAGAGGTTCAATTTTGAAGAAAGGGAACATATATCTCGAAGACAGC	480			
481	CCGTGATCCCAATTCAGTATGCTCTTGAAGCAAAATCACTTTATCTGATGAG	540			
481	CCGTGATCCCAATTCAGTATGCTCTTGAAGCAAAATCACTTTATCTGATGAG	540			
541	GAAATACAGCTGAGGGGACTTGCTGCTCACTTTGAATAGATATGAGCACTGATGAT	600			
541	GAAATACAGCTGAGGGGACTTGCTGCTCACTTTGAATAGATATGAGCACTGATGAT	600			
601	GAAAACTGATACAGTTTACCTGAGCTGATTTGCTGCTCAAGGCTTCATCTG	660			
601	GAAAACTGATACAGTTTACCTGAGCTGATTTGCTGCTCAAGGCTTCATCTG	660			
661	ATGGGATACGTGCATCGAGACATCAAGCTGAGAACTTCTGTTGACCGACAGGAC	720			
661	ATGGGATACGTGCATCGAGACATCAAGCTGAGAACTTCTGTTGACCGACAGGAC	720			
721	ATCAAGCTGATGATTTTGAATCTGCGCGGAAATGAATTCAAACAGATGATGATGCC	780			
721	ATCAAGCTGATGATTTTGAATCTGCGCGGAAATGAATTCAAACAGATGATGATGCC	780			
781	AACTTCCTGATGAGGACCCAGATTAACATGCTCTGAAAGTGCATGATGAACGGG	840			
781	AACTTCCTGATGAGGACCCAGATTAACATGCTCTGAAAGTGCATGATGAACGGG	840			
841	GATGAAAAAGGACCTAAGGCTGAGCTGTGATGATGATGATGATGATGATGATGATGAT	900			
841	GATGAAAAAGGACCTAAGGCTGAGCTGTGATGATGATGATGATGATGATGATGATGAT	900			
901	GAGATGATTTATGAGAGATCCCTCTGCAAGGAACTTCTGCAAGCTTCAATAC	960			
901	GAGATGATTTATGAGAGATCCCTCTGCAAGGAACTTCTGCAAGCTTCAATAC	960			
961	ATTATGATTTCCAGCGGTTTTTGAATTTCAATGACCCCAAGTACAGTACCTT	1020			

Db	961	ATTAGAAATTTCCACGGGTTTTTGAATTTCCAGATGACCCCAAGTAGAGACGACTTT	1020
Qy	1021	CTTGATCTGATTTCAAAGCTGTGTGGCCGGCCAGAAAGAGACTGAATTTGAAGCTTT	1080
Db	1021	CTTGATCTGATTTCAAAGCTGTGTGGCCGGCCAGAAAGAGACTGAATTTGAAGCTTT	1080
Qy	1081	TGCTGCCATCCCTTTCTCTCAAAATTTGACTGGAAACAATTCTGTAACCTCTCCCCC	1140
Db	1081	TGCTGCCATCCCTTTCTCTCAAAATTTGACTGGAAACAATTCTGTAACCTCTCCCCC	1140
Qy	1141	TTTCGTTCCCACTTCAGTCTGACATGACATCTTCGCAATTTTGTATGAACCGAGAAAGAT	1200
Db	1141	TTTCGTTCCCACTTCAGTCTGACATGACATCTTCGCAATTTTGTATGAACCGAGAAAGAT	1200
Qy	1201	TCGTGGGTTTTATCTCTCCGTCGAGCTGAGCCCCCAGGCTTCTCGGGTGAAGAACTG	1260
Db	1201	TCGTGGGTTTTATCTCTCTCCGTCGAGCTGAGCCCCCAGGCTTCTCGGGTGAAGAACTG	1260
Qy	1261	CCGTTTGTGGGGTTTTCGTACAGCAAGGCACTGGGGATTTCTTGTAGATCTGAGTCTGTT	1320
Db	1261	CCGTTTGTGGGGTTTTCGTACAGCAAGGCACTGGGGATTTCTTGTAGATCTGAGTCTGTT	1320
Qy	1321	GTTGTCGGGCTCTGAGACTCCCTCCGCCAGACTGAGCCCCCTAGGCTTCTCGGGTGAAGAACTG	1380
Db	1321	GTTGTCGGGCTCTGAGACTCCCTCCGCCAGACTGAGCCCCCTAGGCTTCTCGGGTGAAGAACTG	1380
Qy	1381	AGCAAAGAGCTACAAAGACTCTCAGGACAAAGTGTACAAGATGGAGACGAAATGACCCGG	1440
Db	1381	AGCAAAGAGCTACAAAGACTCTCAGGACAAAGTGTACAAGATGGAGACGAAATGACCCGG	1440
Qy	1441	TTTCACTCGGAGAGTGTCAAGAGTGGAGGCTGTGCTTACTGACAAAGAGTGGAGCTGAA	1500
Db	1441	TTTCACTCGGAGAGTGTCAAGAGTGGAGGCTGTGCTTACTGACAAAGAGTGGAGCTGAA	1500
Qy	1501	GCTCTGAGACTCAGAGATCCCTCCTCGAGACGAACTTGTCTACCTACATCAAGAATGC	1560
Db	1501	GCTCTGAGACTCAGAGATCCCTCCTCGAGACGAACTTGTCTACCTACATCAAGAATGC	1560
Qy	1561	AGTAGCTTAAAGCCAAAGTTTGGAGCAAGACAGGATGAGGTGTCCCGAGAGATGACAAA	1620
Db	1561	AGTAGCTTAAAGCCAAAGTTTGGAGCAAGACAGGATGAGGTGTCCCGAGAGATGACAAA	1620
Qy	1621	GCACTGCACTCTTCCTCATGATATCAGAGACGAGCCCGAAGCTTCCAAGAAATCAAAGAG	1680
Db	1621	GCACTGCACTCTTCCTCATGATATCAGAGACGAGCCCGAAGCTTCCAAGAAATCAAAGAG	1680
Qy	1681	CAGAGATACAGGCTCAAGTGGAAAGAAATGAGTTGATGATGAATCAAGTTGGAAGAGAT	1740
Db	1681	CAGAGATACAGGCTCAAGTGGAAAGAAATGAGTTGATGATGAATCAAGTTGGAAGAGAT	1740
Qy	1741	CTTGCTTCAGAGAAAGACGAGATGATCTTACGAAATTTGAGCTGAGAGACTCTCGGCTT	1800
Db	1741	CTTGCTTCAGAGAAAGACGAGATGATCTTACGAAATTTGAGCTGAGAGACTCTCGGCTT	1800
Qy	1801	GCTCTGGAAGAAATTCAGCGGAAAGACGACAGATGTGAGCATTAATCTTTGAAGGCTTAAG	1860
Db	1801	GCTCTGGAAGAAATTCAGCGGAAAGACGACAGATGTGAGCATTAATCTTTGAAGGCTTAAG	1860
Qy	1861	GATCAAGGGAAGCCTGAAAGTGGAGAAATATGCGAAATCGAGAAATCAATGCTGAGCAG	1920
Db	1861	GATCAAGGGAAGCCTGAAAGTGGAGAAATATGCGAAATCGAGAAATCAATGCTGAGCAG	1920
Qy	1921	CAGCTCAAAATTTCAAGAGACTCCAGAGAAATCTGAGAAAGGCTCGCAAGAGACCGCAG	1980
Db	1921	CAGCTCAAAATTTCAAGAGACTCCAGAGAAATCTGAGAAAGGCTCGCAAGAGACCGCAG	1980
Qy	1981	AGGAGCTGAGAAAGCTCAGAACCGAGAGAAATTTCTTGAAGGATCAGAAAGAAAGCTG	2040
Db	1981	AGGAGCTGAGAAAGCTCAGAACCGAGAGAAATTTCTTGAAGGATCAGAAAGAAAGCTG	2040
Qy	2041	GTTGAAGCTGAGAAAGCCGCGCATTTCTTGTGAGAACAGATTAAGAGACTGAGACCATG	2100

Db	2041	GTGGAGCTGAGAAACGCCCATTTCTCTGGAGAACAAAGTTAAAGACTTGAAGACCATG	2100
QY	2101	GAGCGTAGAGAAAACAGACTGAGAGATGACATCCAGACAAATATCCCAACAGATCCAGAG	2168
Db	2101	GAGCGTAGAGAAAACAGCTGAAAGATGACATCCAGACAAATATCCCAACAGATCCAGAG	2168
QY	2161	ATGCGTGTAAATTTCTGGAGCTCGAAGAGAAACATGGGAGGCCCAAGTTCAGCCCG	2220
Db	2161	ATGCGTGTAAATTTCTGGAGCTCGAAGAGAAACATGGGAGGCCCAAGTTCAGCCCG	2220
QY	2221	CACCTAGAGTGCACCTGAAACAAAGAGAGAGACTATGAGAAAAGATTAAAGTGTG	2280
Db	2221	CACCTAGAGTGCACCTGAAACAAAGAGAGAGACTATGAGAAAAGATTAAAGTGTG	2280
QY	2281	GACAAATCAGATPAAAGAAAGACCTGGCTGACAAAGAGACACTGGAGAAACATGATCAGAGA	2340
Db	2281	GACAAATCAGATPAAAGAAAGACCTGGCTGACAAAGAGACACTGGAGAAACATGATCAGAGA	2340
QY	2341	CACGAGAGAGAGGCCCATGAGAGAGGCAGAAATTTCTCAGCGAACAGAGGCGATGATCAAT	2400
Db	2341	CACGAGAGAGAGGCCCATGAGAGAGGCAGAAATTTCTCAGCGAACAGAGGCGATGATCAAT	2400
QY	2401	GCTATGATTCCAAGATCAAGATCCCTCGAACAGAGATTGGGAACTGTCTGAAGCCAT	2460
Db	2401	GCTATGATTCCAAGATCAAGATCCCTCGAACAGAGATTGGGAACTGTCTGAAGCCAT	2460
QY	2461	AAACTTGCAGCAAAATAGCAGTCTTTTAAACCAAGAAACATGAGAGGCCCAAGAGAGATG	2520
Db	2461	AAACTTGCAGCAAAATAGCAGTCTTTTAAACCAAGAAACATGAGAGGCCCAAGAGAGATG	2520
QY	2521	ATTTCTGAATCAGGCAACAGAAAATTTTACCTGAGACACAGGCTGGAAATTGAGAGCC	2580
Db	2521	ATTTCTGAATCAGGCAACAGAAAATTTTACCTGAGACACAGGCTGGAAATTGAGAGCC	2580
QY	2581	CAGAACCGAAAACTGGAGAGACAGCTGAGAAATCAAGCCACCAAGACACACATGACAG	2640
Db	2581	CAGAACCGAAAACTGGAGAGACAGCTGAGAAATCAAGCCACCAAGACACACATGACAG	2640
QY	2641	AATGGGCTGCTGGAACCTGGAGACAAAGATTGGGGAGGTCAGTCTAGAGACAGAGAGCAG	2700
Db	2641	AATGGGCTGCTGGAACCTGGAGACAAAGATTGGGGAGGTCAGTCTAGAGACAGAGAGCAG	2700
QY	2701	AAACTGAGCTCAAGCGCCAGCTACAGAGCTACAGTCTTCCCTGCAGAGAGCGGAGTCA	2760
Db	2701	AAACTGAGCTCAAGCGCCAGCTACAGAGCTACAGTCTTCCCTGCAGAGAGCGGAGTCA	2760
QY	2761	CAGTTGACAGCCCTGACAGGCTGACACGGGCGGCCCTTGGAGAGCCAGCTTCCGACGGAG	2820
Db	2761	CAGTTGACAGCCCTGACAGGCTGACACGGGCGGCCCTTGGAGAGCCAGCTTCCGACGGAG	2820
QY	2821	ACAGAGCTGGAAGAGACCAACAGAGAAAGCTGAAGAGATCCAGGCACTCAGGCAACAT	2880
Db	2821	ACAGAGCTGGAAGAGACCAACAGAGAAAGCTGAAGAGATCCAGGCACTCAGGCAACAT	2880
QY	2881	AGAGATGAAATCCAGCGCAATTTTGAAGTCTTTCGTAAACAGCTGTACTGTAAACAGAC	2940
Db	2881	AGAGATGAAATCCAGCGCAATTTTGAAGTCTTTCGTAAACAGCTGTACTGTAAACAGAC	2940
QY	2941	CTGAGAGAGACGCTPAAACACGCTGACCGAGAGCAACGCTGAATCTCAACACCAAACTTC	3000
Db	2941	CTGAGAGAGACGCTPAAACACGCTGACCGAGAGCAACGCTGAATCTCAACACCAAACTTC	3000
QY	3001	TACTTGTCCAAACAACTCGATGAGGCTTTCGGGCGCCAAACGACGAGATTGTACAACTGGA	3060
Db	3001	TACTTGTCCAAACAACTCGATGAGGCTTTCGGGCGCCAAACGACGAGATTGTACAACTGGA	3060
QY	3061	AGTGAAGTGAACCATCTCCGCGGAGATGACGGAACGAGAGATGACGCTTACCAAGCCAG	3120
Db	3061	AGTGAAGTGAACCATCTCCGCGGAGATGACGGAACGAGAGATGACGCTTACCAAGCCAG	3120
QY	3121	AAGCAAAACGATGAGGCTCTGAGAGACACGCTGACCATGCTGGAGAAACAGGTCATGGAT	3180
Db	3121	AAGCAAAACGATGAGGCTCTGAGAGACACACGCTGACCATGCTGGAGAAACAGGTCATGGAT	3180

QY 3181 TTGAGGCGCTTAAACGATGAGCTGCTAGAAAAAGCGGAGTGGAGGCGCTGGAGAGC 3240
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QY 3241 GTCCCTGGGTATGAGAAATCCAGTTTGAAGTGTGGGTGGAGAGCTGAGAAATGCTG 3300
Db 3241 GTCCCTGGGTATGAGAAATCCAGTTTGAAGTGTGGGTGGAGAGCTGAGAAATGCTG 3300
QY 3301 GACCCGAGAAACAGAGCAGGCGAGAGCGGATCAGCCAGTCCAGAGTCCGCAAGT 3360
Db 3301 GACCCGAGAAACAGAGCAGGCGAGAGCGGATCAGCCAGTCCAGAGTCCGCAAGT 3360
QY 3361 GTGGAGCTGGCAGTGAAGAGAGCAAGGCTGAGATTCTCGCTTGCAGAGCGCTTCGAA 3420
Db 3361 GTGGAGCTGGCAGTGAAGAGAGCAAGGCTGAGATTCTCGCTTGCAGAGCGCTTCGAA 3420
QY 3421 GAGCAGAGAGCTGAAGGCGGAGAGCTCTGACAGAGCTCAATGACCTGGAGAGAGCAT 3480
Db 3421 GAGCAGAGAGCTGAAGGCGGAGAGCTCTGACAGAGCTCAATGACCTGGAGAGAGCAT 3480
QY 3481 GCTATGCTTGAATGAAATGATGCGGAGAGCTTACAGCAGAGCTGAGACTGAACGAGGCTC 3540
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QY 3541 AAAACAGAGGCTTGGAGAGAGCAAGCGCAATTACAGCAGAGATGAGCCTGCAGAAAT 3600
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QY 3601 CACATTTTCCGTCTGACTCAGAGAGCTGCAAGAGCTCTAGATCGGAGCTATCTAAG 3660
Db 3601 CACATTTTCCGTCTGACTCAGAGAGCTGCAAGAGCTCTAGATCGGAGCTATCTAAG 3660
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QY 3721 AAGGTGAAATGGAAGAGCAATTTTCTCAACAAACCAATCATTTGATTTTCTGAGAGC 3780
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QY 3781 AAAATGAGCAACCTGCTTAAAAAGAAAGGTTTATTTTATGTCGACGAGAAAGAGCCT 3840
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Db 3901 AAAAGCTCGTGTGACAGAGCTAGAGAGGCTTCAAGAAACCCGATCGAGCTCCGATC 3960
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QY 4021 ACCCGAGAGCAGACATGCGCATGTCCGCAATCGTGGAGTCCGCGAGAGCAGCCAGT 4080
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QY 4081 GCCATGAGCTGTGCTGGCCCGCATCCAGCGGCAAGAAAGAGTCTTCAACTCCAGAGGAA 4140
Db 4081 GCCATGAGCTGTGCTGGCCCGCATCCAGCGGCAAGAAAGAGTCTTCAACTCCAGAGGAA 4140
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Db 4141 TTTAGTCCGCGCTTTAAGAAACGATGACCAATATTTCTCAACCCGATTCAGATGAGA 4200
QY 4201 CTGAAACATGCGAGCCAAAGATGTGCTGTGTCTGATACCGTGCACCTTGGACGCGAG 4260
Db 4201 CTGAAACATGCGAGCCAAAGATGTGCTGTGTCTGATACCGTGCACCTTGGACGCGAG 4260

QY 4261 GCATCCAAATGTCTCGAATGTCAGGATGATGTGTCAACCCCAAGTGTCCAGTGTGCCA 4320
Db 4261 GCATCCAAATGTCTCGAATGTCAGGATGATGTGTCAACCCCAAGTGTCTCAAGTGTGCCA 4320
QY 4321 GCCACTGGGCTTGTGCTGTGATATATGCAACACTTACCGAGGCTTCTCCGCTGAC 4380
Db 4321 GCCACTGGGCTTGTGCTGTGATATATGCAACACTTACCGAGGCTTCTCCGCTGAC 4380
QY 4381 AAAATGAATCTCCGAGGCTCTCCAGACCAAGAGGCCACAGAGGTTCCACTGGAAGG 4440
Db 4381 AAAATGAATCTCCGAGGCTCTCCAGACCAAGAGGCCACAGAGGTTCCACTGGAAGG 4440
QY 4441 TGAATGAAGTGTCCAGAGAAATTAACAAGAGACAGAAAGCTGGAGCAGGAATGACAT 4500
Db 4441 TGAATGAAGTGTCCAGAGAAATTAACAAGAGACAGAAAGCTGGAGCAGGAATGACAT 4500
QY 4501 GTCCCTGGAGGATCAAAAGTCTCTATTTATGACATGAGCCAGAGAGCTGGACAGAG 4560
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QY 4561 CCGGTGAAGAAATTTGAGCTGTGCTCCGACGGGAGTATCTATTCATGTGCGGT 4620
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QY 4741 CCTTCACTGACAGAGT 4800
Db 4741 CCTTCACTGACAGAGT 4800
QY 4801 TTGAAAACTCCCTTAACCAATGTCAGAGAAATTTGAGACAGTCTTCCAAATTTATATATC 4860
Db 4801 TTGAAAACTCCCTTAACCAATGTCAGAGAAATTTGAGACAGTCTTCCAAATTTATATATC 4860
QY 4861 AAGGACCTGAGAGAGCTACTATGATGACAGAGAGAGGCGGACATGTGCTTGTGGAC 4920
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QY 4921 GTGAAGAAAGTGAACAGTCCCTGAGCCAGTCCCACTGCTGCTGCGCCAGCATCTCA 4980
Db 4921 GTGAAGAAAGTGAACAGTCCCTGAGCCAGTCCCACTGCTGCTGCGCCAGCATCTCA 4980
QY 4981 CCCAATCTTTTGAAGCTGTCAAGGCTGCACTTTTGGGGCAGGCAAGATTGAGAAC 5040
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QY 5041 GGGCTGTGATCTGTGAGCCATGCGCAAGAGTGTGATTTCTCGGCTACAAAGAAAC 5100
Db 5041 GGGCTGTGATCTGTGAGCCATGCGCAAGAGTGTGATTTCTCGGCTACAAAGAAAC 5100
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Db 5341 GAGTACTGTGTTTCCAGAAATTTGAGTGTGTGATTTCTTAACGAAAGACGTAGC 5400
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Db 5521 GGGACCCCTGCCCCGAGCGTACTGAGATCCCGAACCCGCTACTGAGCCCTGACAT 5580
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Qy 6181 GCGAATTTATGATCTTCTGAGACGTGAGACTTAATAAATGCGCTTAAGGCTGAGAGC 6240
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RESULT 4
US-10-325-430-11
; Sequence 11, Application US/10325430
; Publication No. US20030153525A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Siles-Santiago, Immaculada
; APPLICANT: Rosenfeld, Julie Beth
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
; FILE REFERENCE: MP101-294PIRM
; CURRENT APPLICATION NUMBER: US/10/325,430
; PRIORITY FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/341,953
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6162
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (1)...(6162)
US-10-325-430-11

Query Match 93.7%; Score 6162; DB 16; Length 6162;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 79 GCCAGCCGGGCTCCAGGCTGATCTGTTTCAAGGAGAAACAACCTTTATGACTCA 138
Db 61 GCCAGCCGGGCTCCAGGCTGATCTGTTTCAAGGAGAAACAACCTTTATGACTCA 120
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Qy 199 GAATGAGTCAAGCTGCTGATGAGATTAAGACGTGAGCACTTTGTCGGAATAT 258
Db 181 GAATGAGTCAAGCTGCTGATGAGATTAAGACGTGAGCACTTTGTCGGAATAT 240
Qy 259 TCCGACACCATAGCTGATTAAGAGAGTCCAGCTTCCGCAAGGACTTCAAGTCA 318
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QY 619 TACCTAGCTGAGCTGATTTTGGCTGTTCAAGGTTTCATGTATGGAGATCGTGATCGA 678
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Db 1621 GATATCAGAGACAGAGCCCGGAAGCTCCAGAAATTCAAAGAGCAGAGATCCAGGCTCA 1680
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QY 1699 GTGAAAGAAATAGGTTGATGATGATGATCAATGTGAAAGAGATCTTGTCTCAGCAAGAA 1758
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QY 1759 CGGATGATCTCTTACGAATCTGAGCTGAGAGAGTCTGGCTTGTCTGAAAGATTCAG 1818
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QY 2179 GAGCTCGAAGAAACATCGGAGGCGCAAGTCTCAGCCGACACTGAAAGTGCACCTG 2238
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Db 2281 GACCTGCTGACAGAGAGACCTGAGAACATGATGACAGAGACCGAGGAGGCGCCAT 2340
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QY 2359 GAGAAAGGCAAAATTTCTCAGCGAACAGAAAGCGATGATCAATGCTATGATTTCCAAATC 2418
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Db 2341 GAGAAAGGCAAAATTTCTCAGCGAACAGAAAGCGATGATCAATGCTATGATTTCCAAATC 2400
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| | | | |
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Db 4741 GTTGT 4800
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Db	481	CAGTATGCGCTTTCAGAGCAAAAATACCTTTATCTGATGAGAGAAATATCAGCTGAGAGG	540
OY	559	GACTTGCTGTCACTTTTGATATGATATAGAGCAGTAGTAGATGAAATCCTGATACAGTTT	618
Db	541	GACTTGCTGTCACTTTTGATATGATATGAGACCAAGTTATGATGAAATCCTGATACAGTTT	600
OY	619	TAAGTAACTGAGCTGATATTTGGCTGTTCACAGCGTTCACTTGATGGATATACGTGATCGA	678
Db	601	TAAGTAACTGAGCTGATATTTGGCTGTTCACAGCGTTCACTTGATGGATATACGTGATCGA	660
OY	679	GAGATCAAGCCCTGAGAACATTCGTGTACCGGACAGGACATCAACCTGCTGATATTT	738
Db	661	GAGATCAAGCCCTGAGAACATTCGTGTACCGGACAGGACATCAACCTGCTGATATTT	720
OY	739	GGATCTGCGCGGAAAAATGATTCAAACAAGATGTGAAATGGCCAACTCCGATTTGGAGC	798
Db	721	GGATCTGCGCGGAAAAATGATTCAAACAAGATGTGAAATGGCCAACTCCGATTTGGAGC	780
OY	799	CCAAGTTACATGCGCTCTGAAAGTGTGACTGTGATGAAACGGGATATGAAAAAGGCACTTAC	858
Db	781	CCAAGTTACATGCGCTCTGAAAGTGTGACTGTGATGAAACGGGATATGAAAAAGGCACTTAC	840
OY	859	GGCCCTGAGCTGTGATGTGATGTGACAGTGGGCGGATTTGCTTATGAGATATTTATGGAGAG	918
Db	841	GGCCCTGAGCTGTGATGTGATGTGACAGTGGGCGGATTTGCTTATGAGATATTTATGGAGAG	900
OY	919	TCGCCCTTTCGACAGAGGAACTCTGCGCAAACTTCAATPAACATTATGAAATTTCCAGCGG	978
Db	901	TCGCCCTTTCGACAGAGGAACTCTGCGCAAACTTCAATPAACATTATGAAATTTCCAGCGG	960
OY	979	TTTTTGAAATTTCCAGATGACCCCAAGATGAGAGCTGCTTCTTGATCTGATTCAAAGC	1038
Db	961	TTTTTGAAATTTCCAGATGACCCCAAGATGAGAGCTGCTTCTTGATCTGATTCAAAGC	1020
OY	1039	TTGTTGTGCGGCGCAGAAAAGAGAGACTGAAAGTTTGAAGCTCTTGTGCGCATCCTTTCTTC	1098
Db	1021	TTGTTGTGCGGCGCAGAAAAGAGAGACTGAAAGTTTGAAGCTCTTGTGCGCATCCTTTCTTC	1080
OY	1099	TCTTAAAAATTGACTGGAACAACATCTGTAACTCTCTCCCCCTTGTGTTCCACCTCAAG	1158
Db	1081	TCTTAAAAATTGACTGGAACAACATCTGTAACTCTCTCCCCCTTGTGTTCCACCTCAAG	1140
OY	1159	TCTGACATGACACCTCCCAATTTTGATGAACAAGAGAAATGCGTGGGTTTCAATCCCTC	1218
Db	1141	TCTGACATGACACCTCCCAATTTTGATGAACAAGAGAAATGCGTGGGTTTCAATCCCTC	1200
OY	1219	CCGTGCGAGCTGAGGCCCTCAAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCG	1278
Db	1201	CCGTGCGAGCTGAGGCCCTCAAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCG	1260
OY	1279	TACAGCAAGGCACTGGGGGATCTTGGTATGATCTGATCTGTGTGTGGGCTGTGAATCCG	1338
Db	1261	TACAGCAAGGCACTGGGGGATCTTGGTATGATCTGATCTGTGTGTGGGCTGTGAATCCG	1320
OY	1339	CCTGCGCAAGACTAGCTCCATGGAAGAACTTCTCATCAAAAGCAAGACTCAAGAC	1398
Db	1321	CCTGCGCAAGACTAGCTCCATGGAAGAACTTCTCATCAAAAGCAAGACTCAAGAC	1380
OY	1399	TCTTCAGAGCAAGTGTCAACAATGGAAGCAAGAAATGACCCGGTTTACATCGGAGAGTGTCA	1458
Db	1381	TCTTCAGAGCAAGTGTCAACAATGGAAGCAAGAAATGACCCGGTTTACATCGGAGAGTGTCA	1440
OY	1459	GAGGTGAGAGCTGTGCTTGTAGTCAAGAGAGGCTGAGAGGCTCTGAGACTCAAGAG	1518
Db	1441	GAGGTGAGAGCTGTGCTTGTAGTCAAGAGAGGCTGAGAGGCTCTGAGACTCAAGAG	1500
OY	1519	TCCCTCTCTGAGAGGAACTTGTCTACTTACATCAACAGATGAGTACTTAAAGGAAAGT	1578
Db	1501	TCCCTCTCTGAGAGGAACTTGTCTACTTACATCAACAGATGAGTACTTAAAGGAAAGT	1560

QY	1579	TTGAGCAAGACCGAGTGAAGTCTCCACGAGAGATGACAAAGACTGACGCTTCTCCAT	1638
Db	1561	TTGGAGCAAGACCGAGTGAAGTGTCTCCACGAGAGATGACAAAGACTGACACTTCTCCAT	1620
QY	1639	GATATCAAGAGCAGAGCGCGGAGCTCCAAAGAAATCAAAGACAGAGATCACAGCTCAA	1698
Db	1621	GATATCAAGAGCAGAGCGCGGAGCTCCAAAGAAATCAAAGACAGAGATCACAGCTCAA	1680
QY	1699	GTGGAGAAATGAGGTTGATGATGAATCATGTTGAGAGAGATCTTGTCTCAGCAAGAGA	1758
Db	1681	GTGGAGAGAAATGAGGTTGATGATGAATCATGTTGAGAGAGATCTTGTCTCAGCAAGAGA	1740
QY	1799	CGGAGTGAATCTCTACGAATCTGAGCTGAGAGAGTCTCGGCTTGTGCTGTGAAGAAATTCAG	1818
Db	1741	CGGAGTGAATCTCTACGAATCTGAGCTGAGAGAGTCTCGGCTTGTGCTGTGAAGAAATTCAG	1800
QY	1819	CGGAAAGCGACAGAGATGTACGATTAATCTGTGAAGGCTAAGAGATCAAAGGAGACCTGAA	1878
Db	1801	CGGAAAGCGACAGAGATGTACGATTAATCTGTGAAGGCTAAGAGATCAAAGGAGACCTGAA	1860
QY	1879	GTGGAGAAATATGCGAAACTGAGAGAGATCAATCTGACGACAGCTCAAAAATTCAGAG	1938
Db	1861	GTGGAGAAATATGCGAAACTGAGAGAGATCAATCTGACGACAGCTCAAAAATTCAGAG	1920
QY	1939	CTCCAAAGAAACTGAGAGAGGCTTCCAAAGAGCGAGCCGAGAGAGACTGAGAGAGCTG	1998
Db	1921	CTCCAAAGAAACTGAGAGAGGCTTCCAAAGAGCGAGCCGAGAGAGACTGAGAGAGCTG	1980
QY	1999	CAGAACCGAGAGGATTTCTTCTGAAGGCAATCGAAGAAAGAGCTGATGGAAGCTGAGAAAGC	2058
Db	1981	CAGAACCGAGAGGATTTCTTCTGAAGGCAATCGAAGAAAGAGCTGATGGAAGCTGAGAAAGC	2040
QY	2059	CGCCATTTCTCTGAGGAACAAGTAAAGAGACTAGAGACCATGAGCGTGAAGAGAAACAGA	2118
Db	2041	CGCCATTTCTCTGAGGAACAAGTAAAGAGACTAGAGACCATGAGCGTGAAGAGAAACAGA	2100
QY	2119	CTGAAGAGTGAATTCACGACAAATTCACACAGATCCAGAGATGCTGATAAATTTCTG	2178
Db	2101	CTGAAGAGTGAATTCACGACAAATTCACACAGATCCAGAGATGCTGATAAATTTCTG	2160
QY	2179	GAGCTCGAAGAGAAACAATCGGAGAGGCCAAGTCTCACCCAGACCTTAAGAGTGCACCTG	2238
Db	2161	GAGCTCGAAGAGAAACAATCGGAGAGGCCAAGTCTCACCCAGACCTTAAGAGTGCACCTG	2220
QY	2239	AAACAGAAAGAGCAGCACTATGAGAGAAAGATTAAAGTTTGAGCAATTCAGATTAAGAAA	2298
Db	2221	AAACAGAAAGAGCAGCACTATGAGAGAAAGATTAAAGTTTGAGCAATTCAGATTAAGAAA	2280
QY	2299	GACCTGCTGACAAAGAGACACTGAGAGACATGATGACAGAGACACGAGAGAGAGGCCAT	2358
Db	2281	GACCTGCTGACAAAGAGACACTGAGAGACATGATGACAGAGACACGAGAGAGAGGCCAT	2340
QY	2359	GAGAAAGGCGAAATTTCTCAGCGAACACAGAGGCCATGATCAATGCTATGATTTCCAAAGTC	2418
Db	2341	GAGAAAGGCGAAATTTCTCAGCGAACACAGAGGCCATGATCAATGCTATGATTTCCAAAGTC	2400
QY	2419	AGATCCCTCGAAGCAGAGGATGTGGAACCTGTCAAGCGCAATTAACCTTGACGCAAAATAGC	2478
Db	2401	AGATCCCTCGAAGCAGAGGATGTGGAACCTGTCAAGCGCAATTAACCTTGACGCAAAATAGC	2460
QY	2479	AGTCTTTTATCCAAAGGACATGAGAGGCCCCAGAGAGAGATGATTTCTGAATCTGAGCAA	2538
Db	2461	AGTCTTTTATCCAAAGGACATGAGAGGCCCCAGAGAGAGATGATTTCTGAATCTGAGCAA	2520
QY	2539	CAGAAATTTTATCTTGAAGACACAGGCTGCGGAAGTTGAGAGCCCGAGAACCTGAGAAC	2598
Db	2521	CAGAAATTTTATCTTGAAGACACAGGCTGCGGAAGTTGAGAGCCCGAGAACCTGAGAAC	2580
QY	2599	GAGCAGCTGAGAGAGATCAGCCACCAAGACCAACAGTGAACAAGATCGGCTGCTGGAACCTG	2658
Db	2581	GAGCAGCTGAGAGAGATCAGCCACCAAGACCAACAGTGAACAAGATCGGCTGCTGGAACCTG	2640
QY	2659	GAGCAGAGATTTGCGGAGGCTCAGTCTAGAGCACGAGAGCAGAAATCTGAGCTCAAGCGC	2718

Db 2641 GAGACAAGATTGGGGAGGTCAAGTCTAGAGCAGAGAGAGAAACTGGAGCTCAAGCCG 2700
QY 2719 CAGCTCACAGAGTATAGCTTCTCCCTGCGAGAGCGGAGTCAAGTTTGAACGCCCTGCGAG 2778
Db 2701 CAGCTCACAGAGTATAGCTTCTCCCTGCGAGAGCGGAGTCAAGTTTGAACGCCCTGCGAG 2760
QY 2779 GCTGCACGGGCGGCTCTGGAGAGCCAGCTTCGCGCAGGCGGAGACAGAGCTGGAAAGAGCC 2838
Db 2761 GCTGCACGGGCGGCTCTGGAGAGCCAGCTTCGCGCAGGCGGAGACAGAGCTGGAAAGAGCC 2820
QY 2839 ACGAGCAAGAGCTGAAAGAGAGATCCAGGCACTCAACGCAATAGATGAATCCAGCCG 2898
Db 2821 ACGAGCAAGAGCTGAAAGAGAGATCCAGGCACTCAACGCAATAGATGAATCCAGCCG 2880
QY 2899 AATATTGATGCTCTTGTGTAACAGCTGTACTGTATATCAAGACTGGAGAGCAGCTTAAC 2958
Db 2881 AATATTGATGCTCTTGTGTAACAGCTGTACTGTATATCAAGACTGGAGAGCAGCTTAAC 2940
QY 2959 CAGCTGACCGAGAGCAACGCTGAACTCAACAACCAAACTTCTACTTGTCCAAAACAATC 3018
Db 2941 CAGCTGACCGAGAGCAACGCTGAACTCAACAACAACCAAACTTCTACTTGTCCAAAACAATC 3000
QY 3019 GATGAGGCTTCTGGCGCCCAACGAGATTGTACAACTGCGAAGTGAAGTGAACATCTC 3078
Db 3001 GATGAGGCTTCTGGCGCCCAACGAGATTGTACAACTGCGAAGTGAAGTGAACATCTC 3060
QY 3079 CCGCGGGAATATACCGGAAGAGAGATGCGAGCTTACCGAGCAGAAAGCAATGAGGCT 3138
Db 3061 CCGCGGGAATATACCGGAAGAGAGATGCGAGCTTACCGAGCAGAAAGCAATGAGGCT 3120
QY 3139 CTGAAGACCAAGTGCACATGCTGAGAGAACAGTATGATTTTGGAGGCCCTTAACGAT 3198
Db 3121 CTGAAGACCAAGTGCACATGCTGAGAGAACAGTATGATTTTGGAGGCCCTTAACGAT 3180
QY 3199 GAGCTGCTAGAAAAGAGCGGCGAGTGGAGGCTTGGAGAGCGTCTGAGTATGAGAAA 3258
Db 3181 GAGCTGCTAGAAAAGAGCGGCGAGTGGAGGCTTGGAGAGCGTCTGAGTATGAGAAA 3240
QY 3259 TCCGAGTTGAGTGTGCGGGTTGAGAGCTGCGAGAGAAATGTGAGACCCAGAAAACGAGAC 3318
Db 3241 TCCGAGTTGAGTGTGCGGGTTGAGAGCTGCGAGAGAAATGTGAGACCCAGAAAACGAGAC 3300
QY 3319 AGGGCGAGAGCCGATACAGCGAGTCAACCGAGTCTCGCAGAGTGGAGCTGCGAGTGAAG 3378
Db 3301 AGGGCGAGAGCCGATACAGCGAGTCAACCGAGTCTCGCAGAGTGGAGCTGCGAGTGAAG 3360
QY 3379 GAGCACAAGGCTGAGATTCTCGCTGCGAGCAGGCTCTCAAGAGCAGAAAGCTGAAGGCC 3438
Db 3361 GAGCACAAGGCTGAGATTCTCGCTGCGAGCAGGCTCTCAAGAGCAGAAAGCTGAAGGCC 3420
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Db 3421 GAGAGCTCTGACAAAGCTCAATGACTGAGGAAGAAAGCATGTATGCTTGAATGAAT 3480
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Db 3481 GCCCGAAGCTTACAGCAGAAAGCTGAGATGTAACGAGAGCTCAACAGAGGCTTCTGAA 3540
QY 3559 GAGCAAGCCAAATTACAGCAGAGATGTAACCTGCGAGAAAATCACTTTTCCGCTGACT 3618
Db 3541 GAGCAAGCCAAATTACAGCAGAGATGTAACCTGCGAGAAAATCACTTTTCCGCTGACT 3600
QY 3619 CAAGGCTGCAAGAGCTTAAGTGGGGTGAATCTATCTGAGACAGAAAGAGTGACTTG 3678
Db 3601 CAAGGCTGCAAGAGCTTAAGTGGGGTGAATCTATCTGAGACAGAAAGAGTGACTTG 3660
QY 3679 GAGTATCAAGCTGSAAAACATTCAAGTTCTCTATTCTCATGAAGGAGTGAATGSAAGGC 3738
Db 3661 GAGTATCAAGCTGSAAAACATTCAAGTTCTCTATTCTCATGAAGGAGTGAATGSAAGGC 3720
QY 3739 ACTATTTCGAACAAACCAACTCATTTATTTTCTGCAAGCCAAATGAGCAACCTGCT 3798

Db 3721 ACTATTTCGAACAAACCAACTCATTTATTTTCTGCAAGCCAAATGAGCAACCTGCT 3780
QY 3799 AAAAAAGAAAAGGGTTATTTATGAGCGSAAAGAGAGCCCGCTTTCACCAAGAGTT 3858
Db 3781 AAAAAAGAAAAGGGTTATTTATGAGCGSAAAGAGAGCCCGCTTTCACCAAGAGTT 3840
QY 3859 CCTTCGAGTACAAATGAGAGTGAAGCTGGCCCTGAGAAAGSAAAGAGTCTGCTGACAGAG 3918
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Db 3901 CTAGAGAAAGCCCTTCAAGAAAGCCGCAATCGAGTCCGCTCCGCGGAGAGAGCTGCC 3960
QY 3979 CACCGAAAGCAAGGAGCCAGCCAGACCATCATCAGCCAGCCAGCCAGGAGGAGAGATC 4038
Db 3961 CACCGAAAGCAAGGAGCCAGCCAGACCATCATCAGCCAGCCAGCCAGGAGGAGAGATC 4020
QY 4039 GCCATGTCGCGCATGTCGCGTCCGCAAGAGCACAGCCAGTCCATGAGCTGTCGCC 4098
Db 4021 GCCATGTCGCGCATGTCGCGTCCGCAAGAGCACAGCCAGTCCATGAGCTGTCGCC 4080
QY 4099 CCGCATTCAGCCGCAAGAGAGTCTTCACTCCAGAGAAATTTAGTGCCTTTAAG 4158
Db 4081 CCGCATTCAGCCGCAAGAGAGTCTTCACTCCAGAGAAATTTAGTGCCTTTAAG 4140
QY 4159 GAAAGCATGACCAAAATATCTCAACGATTCAGATGAGATGAGATGAGAGCCACA 4218
Db 4141 GAAAGCATGACCAAAATATCTCAACGATTCAGATGAGATGAGATGAGAGCCACA 4200
QY 4219 AAGTGTGCTGTGTCTGAGATACCGTGCATCTTGGAGCCAGGCAATCCAAATGTCTGAA 4278
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QY 4279 TGTCAAGTGAATGTTCACCCCAAGTGTTCACAGTCTTCCAGCCACTGCGGCTTGCT 4338
Db 4261 TGTCAAGTGAATGTTCACCCCAAGTGTTCACAGTCTTCCAGCCACTGCGGCTTGCT 4320
QY 4339 GGTGAATATGCGACACATTCACCGAGGCGTTCTGCGGTGACAAATGAATCACTCCAGGT 4398
Db 4321 GGTGAATATGCGACACATTCACCGAGGCGTTCTGCGGTGACAAATGAATCACTCCAGGT 4380
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Db 4441 AATTAACCAAGAGCAGCAGAGCTGGGACAGAAAGTCACTTGTCTCTGAGGAGATCAAAA 4500
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QY 4579 CTGTGCTTCCCGAGCGGGAGTGTATCTATTAAGTGTGCGTGTGATCTTCGAACTGCA 4638
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QY 4699 AAACTGAAGAGTGAAGCAGTCTGACATGAACTGACAGCTGCGCTTCAGTGAACAGAGT 4758
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Db 4741 GTGTGTGTGGGACCGAGAGAGGGCTCTACGCCCTGAAATGTCTTGAAGAACTCCCTAAAC 4800
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5179 CTGATTTGAACCAATTAATTTCTAAGAAATGACATGAGAGTACAGCTCGAGAAATTC 5238
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5239 CTGATTAAGATGACATTTCTTGGGACCTGCTGTGTGTTGGCCCTCTTCCACAGCTTC 5298
5221 CTGATTAAGATGACATTTCTTGGGACCTGCTGTGTGTTGGCCCTCTTCCACAGCTTC 5280
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5359 CAAGAATTTGAGGTGTTCTGATTTCTTGAAGAGAGTACCGGACAGAGCATCTCAAG 5418
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5419 TGGAGTCGCTTACCTTTGGCTTGGCTTACAGAGAACCTTATCTGTTTGAAGCACTTC 5478
5401 TGGAGTCGCTTACCTTTGGCTTGGCTTACAGAGAACCTTATCTGTTTGAAGCACTTC 5460
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5581 TTGGCGCTCTCAATCAAGATTAATTTAAGGTGATTTGCTGCAAGAGAAACCTCTGTAAG 5640
5659 GAGTCCGGCACTGAACCAACCGGGGCGGTCCACCTCCCGAGAGAGCCCAACAAGCA 5718
5641 GAGTCCGGCACTGAACCAACCGGGGCGGTCCACCTCCCGAGAGAGCCCAACAAGCA 5700
5719 GGGCCACCAAGTACAGAGCAATCAACCAAGCGGTGGCTTCCAGCCAGCGCGCC 5778
5701 GGGCCACCAAGTACAGAGCAATCAACCAAGCGGTGGCTTCCAGCCAGCGCGCC 5760
5779 GAAAGGCGCCAG 5838
5761 GAAAGGCGCCAG 5820
5839 GAGCTGCGAG 5898
5821 GAGCTGCGAG 5880
5899 ATGCTCAGACAG 5958
5881 ATGCTCAGACAG 5940

QY 5959 CGGCTGCTGCGGAGAGCGGTGAGAGACCCCGCTGTCTCCAGGTGAACAAGGAGAGAG 6018
DB 5941 CGGCTGCTGCGGAGAGCGGTGAGAGACCCCGCTGTCTCCAGGTGAACAAGGAGAGAG 6000
QY 6019 AGTGCCTCTCAAGTTTCAAGGTTTAACTGTCACTTATTAATTAATTAATTAATTA 6078
DB 6001 AGTGCCTCTCAAGTTTCAAGGTTTAACTGTCACTTATTAATTAATTAATTAATTA 6060
QY 6079 GACAACTGCGAGCTGACGTGCTGAGAGATCACTCACTGAATTAATTAATTAATTA 6138
DB 6061 GACAACTGCGAGCTGACGTGCTGAGAGATCACTCACTGAATTAATTAATTAATTA 6120
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DB 6121 CAGAGGTTGAAGAGTCTGTTCTGAGAGAGATTAATTAATTAATTAATTAATTA 6159

RESULT 6
US-10-415-011-43
; Sequence 43, Application US/10415011
; Publication No. US20040053394A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION
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; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: XU, Yuming
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: YAO, Monique G.
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: DING, Li
; APPLICANT: TANG, Y. Tom
; APPLICANT: HAFALIA, April J.A.
; APPLICANT: NGUYEN, Daniel B.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: LU, Yan
; APPLICANT: YUE, Henry
; APPLICANT: BURFORD, Neil
; APPLICANT: BANDMAN, Olga
; APPLICANT: TRIBOULET, Catherine M.
; APPLICANT: LAL, Preeti G.
; APPLICANT: RECIPON, Shirley A.
; APPLICANT: LU, Dzung Aina M.
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; APPLICANT: THORNTON, Michael B.
; APPLICANT: SWARNAXER, Anita
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: KHAN, Farrah A.
; APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0262 USN
; CURRENT APPLICATION NUMBER: US/10/415,011
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; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/247,672
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/249,565
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: US 60/252,730
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/250,807
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PERL Program
; SEQ ID NO 43

LENGTH: 6298
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incycle ID No. US2004005394A1 7484498CB1
US-10-415-011-43

Query Match 86.5%; Score 5684.4; DB 17; Length 6298;
Best Local Similarity 95.3%; Pred. No. 0;
Matches 5979; Conservative 0; Mismatches 36; Indels 243; Gaps 3;

QY 1 AGAGCCCGCAGTGGGAGATGTGAAGTCAAAATATAGAGCGGGATCCTTTGATGCT 60
DB 37 AGAGCCCGCAGTGGGAGATGTGAAGTCAAAATATAGAGCGGGATCCTTTGATGCT 96
QY 61 GGTGCTGCTGAACCCATTCGACCGGGCTCCAGGCTGATCTTTCTTCAGGGGAAA 120
DB 97 GGTGCTGCTGAACCCATTCGACCGGGCTCCAGGCTGATCTTTCTTCAGGGGAAA 156
QY 121 CCAACCTTTATGACTCAAGACAGATGCTCTCTCTTCCCGAAGAGGATTTAGTGC 180
DB 157 CCAACCTTTATGACTCAAGACAGATGCTCTCTCTTCCCGAAGAGGATTTAGTGC 216
QY 181 CTCTTTGCTCTTTGAAGATGCACTGCTCTCTGTAAGATTAAGCACTGAGC 240
DB 217 CTCTTTGCTCTTTGAAGATGCACTGCTCTCTGTAAGATTAAGCACTGAGC 276
QY 241 AACTTGTCCGGAAGTATTCGACACCATAGCTGATTCAGAGCTCCAGCTTCGGCA 300
DB 277 AACTTGTCCGGAAGTATTCGACACCATAGCTGATTCAGAGCTCCAGCTTCGGCA 336
QY 301 AAGCACTTCGAGTCAAGATCTTGTAGGTTGTCACCTTGTCTGAAGTCAGGCTGA 360
DB 337 AAGCACTTCGAGTCAAGATCTTGTAGGTTGTCACCTTGTCTGAAGTCAGGCTGA 396
QY 361 AAGGAGAAAGCAACCGGGGACATCTATGCTATGAAGATGATGAAGAGGCTTATATG 420
DB 397 AAGGAGAAAGCAACCGGGGACATCTATGCTATGAAGATGATGAAGAGGCTTATATG 456
QY 421 GCCAGAGACAGGTTTCATTTTTGAAGAGCGGAATATATATCTTGAAGCACAGC 480
DB 457 GCCAGAGACAGGTTTCATTTTTGAAGAGCGGAATATATATCTTGAAGCACAGC 516
QY 481 CCGTGATCCCCCAATTACAGTATGCTTTCAGGACAAAATCACCTTATCTGATGAG 540
DB 517 CCGTGATCCCCCAATTACAGTATGCTTTCAGGACAAAATCACCTTATCTGATGAG 576
QY 541 GAATATCAGCTCGAGGGGACTTCTGTCTCACTTTGAATGATATGAGGACCAATTAGAT 600
DB 577 GAATATCAGCTCGAGGGGACTTCTGTCTCACTTTGAATGATATGAGGACCAATTAGAT 636
QY 601 GAAAACTGATACAGTTTACCTAGCTGAGTATTTGGCTGTCAAGCGCTTATATCTG 660
DB 637 GAAAACTGATACAGTTTACCTAGCTGAGTATTTGGCTGTGTCAAGCGCTTATATCTG 696
QY 661 ATGGATACGTCATCGAGACATCAAGCTTGAAACATTTCTGTTACCGGACAGAGAC 720
DB 697 ATGGATACGTCATCGAGACATCAAGCTTGAAACATTTCTGTTACCGGACAGAGAC 756
QY 721 ATCAAGCTGATGATTTTGGATCTGCGCGGAAAATGAATTCAAACAAATGCTGATGCC 780
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DB 817 AAACCTCCGATTTGGAGCCCGAGATTACATGGCTCTGAAGTGTGATGATGAGG 876
QY 841 GATGAGAAAGCACTTACGGCTTGAAGTGTGATGATGATGATGATGATGATGATGAT 900
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QY 1081 TCGTCCATCTCTTCTCTTAATTTGATCTGAACCAATTCTGATCTCTCTCC 1140
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QY 1141 TCGTCCATCTCTGATCTGAAGTCACTTCAATTTTGAATGATGATGATGATGAT 1200
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RESULT 7
US-10-618-941-1
; Sequence 1, Application US/10618941
; Publication No. US2004019792A1
; GENERAL INFORMATION:

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1  APPLICANT: WHITE, DAVID
2  APPLICANT: MANNING, GERARD
3  APPLICANT: CAENEPEEL, SEAN
4  TITLE OF INVENTION: NOVEL KINASES
5  FILE REFERENCE: 034536-0321
6  CURRENT APPLICATION NUMBER: US/10/618,941
7  CURRENT FILING DATE: 2003-07-15
8  PRIOR APPLICATION NUMBER: 60/395,632
9  PRIOR FILING DATE: 2002-07-15
10 NUMBER OF SEQ ID NOS: 143
11 SOFTWARE: PatentIn version 3.2
12 SEQ ID NO 1
13     LENGTH: 8656
14     TYPE: DNA
15 ORGANISM: Homo sapiens
16 US-10-618-941-1

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Query Match	86.2%	Score 5669.8	DB 18	Length 8656
Best Local Similarity	95.5%	Pred. No. 0		
Matches 5978; Conservative	0	Mismatches 37	Indels 246	Gaps 4

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QY	121	CCACCCCTTATGACTCAACAGCAGATGTCCTCCTCTTCCCGAAGAGGATATTAGATGCC	180		
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QY	181	CTCTTTGTTCTCTTTGAAAGATGCAAGTCAAGCTGCTCTGATGAAATTAAGACGTGAC	240		
Db	213	CTCTTTGTTCTCTTTGAAAGATGCAAGTCAAGCTGCTCTGATGAAATTAAGACGTGAGC	272		
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Db	273	AACCTTTGTCCCGGAAGTATTCGACACACATAGCTGATTAACAGAGGCTCAGGCTTCG	332		
QY	298	GCAAAAGACTTCGAAAGTCTTGAAGTTGAGTTCGACTTTGCTGAAGTCAGGTG	357		
Db	333	GCAAAAGACTTCGAAAGTCTTGAAGTTGAGTTCGACTTTGCTGAAGTCAGGTG	392		
QY	358	GTAAGAGGAAAGCAACCGGGGACATCTATGCTATGAAAGTGAATAAGAAAGGCTTTA	417		
Db	393	GTAAGAGGAAAGCAACCGGGGACATCTATGCTATGAAAGTGAATAAGAAAGGCTTTA	452		
QY	418	TTGGCCCGAGAGCAGGTTTCATTTTGTAGGAAAGCGGAAACATTTATCTCGAAGCACA	477		
Db	453	TTGGCCCGAGAGCAGGTTTCATTTTGTAGGAAAGCGGAAACATTTATCTCGAAGCACA	512		
QY	478	AGCCCGTGATCCCCCAATTACAGTATGCCITTCAGACAACAATAACCTTATCTGATG	537		
Db	513	AGCCCGTGATCCCCCAATTACAGTATGCCITTCAGACAACAATAACCTTATCTGATG	572		
QY	538	GAGGAATATCAGCTCGAGGGGACTTGCTGTCACTTTGATATGATATGAGGACCAATTA	597		
Db	573	ATGGAATATCAGCTCGAGGGGACTTGCTGTCACTTTGATATGATATGAGGACCAATTA	632		
QY	598	GATGAAACCTGATCAGTTTATCTACTGACTGAGTATTTTGGCGGTTCAACAGCGTCAAT	657		
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QY	838	GGGGATGGAAAAGGACCTACGGCTGTGAAGTGTGACCTGTGTATGACCTGTGTATGAC	897
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QY	898	TATGAGATGATTTATGGAGATGCCCTTCGACAGGGGAACTTCGACAACTTCAT	957
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QY	958	AACTTATGAATTTCCAGCGGTTTTTGAATTTCCAGATGACCCCAAGTGTGAC	1017
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Qy 1918 CAGAGCTCAAAATTTCCAGAGCTCCAAAGAAACTGGAGAGCT----- 1962
Db 1953 CAGAGCTCAAAATTTCCAGAGCTCCAAAGAAACTGGAGAAAGCTGTAAAGCCAGACG 2012
Qy 1963 -----GCCAAGGAGGAGCCCGAGAGAGCTG 1989
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Qy 2890 ATCCAGCGCAAAATTTGATGCTCTTCGTAAAGAGCTGTACTGTAATCAGACACTTGAAGAG 2949

Db 2973 ATCCAGCGCAAAATTTGATGCTCTTCGTAAACAGCTGTACTGTATCAAGACCTGAGAGAG 3032
Qy 2950 CAGCTAAACAGCTGACCGAGAGCAACGCTGAACTCAACCAACAAATCTTCACTTGTC 3009
Db 3033 CAGCTAAACAGCTGACCGAGAGCAACGCTGAACTCAACCAACAAATCTTCACTTGTC 3092
Qy 3010 AAAACACTGATGAGGCTTTGCGGCCCAACGAGAGATTTGAACACTCGAGAGTGAAGTG 3069
Db 3093 AAAACACTGATGAGGCTTTGCGGCCCAACGAGAGATTTGAACACTCGAGAGTGAAGTG 3152
Qy 3070 GACCAATTCGCGCGGAGAGATCAACGGAACGAGAGATGACCTTACAGCCAGAAAGCAACG 3129
Db 3153 GACCAATTCGCGCGGAGAGATCAACGGAACGAGAGATGACCTTACAGCCAGAAAGCAACG 3212
Qy 3130 ATGAGGCTCTGAAAGACACGTCGACACATGCTGAGAGAACAGTCAATGATTTGGAGGCC 3189
Db 3213 ATGAGGCTCTGAAAGACACACGTCGACACATGCTGAGAGAACAGTCAATGATTTGGAGGCC 3272
Qy 3190 CTAAACGATGAGCTCTTGAATAAAGAGCGCAATGAGAGGCTTGAGAGAGCGTCTGGGT 3249
Db 3273 CTAAACGATGAGCTCTTGAATAAAGAGCGCAATGAGAGGCGCTTGAGAGAGCGTCTGGGT 3332
Qy 3250 GATGAGAAATCCCAAGTTTGAAGTTCGAGGTTGAGAGCTGACAGAAATGCTGGAACACCGAG 3309
Db 3333 GATGAGAAATCCCAAGTTTGAAGTTCGAGGTTGAGAGCTGACAGAAATGCTGGAACACCGAG 3392
Qy 3310 AAAACAGACAGAGGCGAGAGCCGATCAGCGGATCAACGAGTCTCCAGAGTGTGAGAGCTG 3369
Db 3393 AAAACAGACAGAGGCGAGAGCCGATCAGCGGATCAACGAGTCTCCAGAGTGTGAGAGCTG 3452
Qy 3370 GCAGTGAAGGAGCAACAGGCTGAGATTTCCGCTTTCGACAGCGCTTCAAGAGACAGAG 3429
Db 3453 GCAGTGAAGGAGCAACAGGCTGAGATTTCCGCTTTCGACAGCGCTTCAAGAGACAGAG 3512
Qy 3430 CTGAAGGCGGAGAGCTCTCTGACAACTCATAGACCTGAGAGAGAGCATGTATGCTT 3489
Db 3513 CTGAAGGCGGAGAGCTCTCTGACAACTCATAGACCTGAGAGAGAGCATGTATGCTT 3572
Qy 3490 GAAATGAATGCCCGAAGCTTACAGCAGAGCTGAGACTGAACGAGAGCTCAACAGAGG 3549
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Qy 3550 CTTCTGGAAGAGCAAGCCAAATTAACAGCAGAGTGAACCTGCAAGAAATTAACATTTTC 3609
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Db 3753 AGTGACTTGAAGTATCAGCTGGAATAACATTCAGGTTCTATATCTCATGAAAAGTGAAA 3812
Qy 3730 ATGGAAGGCACTATTTCTCAACAAACCAACTGATGATTTTCGCAAGCCAAATGAGAC 3789
Db 3813 ATGGAAGGCACTATTTCTCAACAAACCAACTGATGATTTTCGCAAGCCAAATGAGAC 3872
Qy 3790 CAACCTGCTAATAAAGAAAAGGTTATTTAGTCAGCGAAGAGAGACCTTGCTTTAACCC 3849
Db 3873 CAACCTGCTAATAAAGAAA----- 3891
Qy 3850 ACAAGGTTCTCTGAGATCAATGAGCTGAACTGGCCCTTGAGAGAGAGAAAGCTCCG 3909
Db 3892 -----AGGTTCTCTGAGATCAATGAGCTGAACTGGCCCTTGAGAGAGAGAAAGCTCCG 3947
Qy 3910 TGTGAGAGCTTAAGAGAGCCCTTCAAGAGACCCGATCGAGCTCGGTCGCGCGGAGG 3969
Db 3948 TGTGAGAGCTTAAGAGAGCCCTTCAAGAGACCCGATCGAGCTCGGTCGCGCGGAGG 4007
Qy 3970 GAAAGTCCCAACGCAAGCAACGACCAACCACTCAACGCGCAGCCACCGGAGG 4029
Db 4008 GAAAGTCCCAACGCAAGCAACGACCAACCACTCAACGCGCAGCCACCGGAGG 4067

OY	4030	CAGCAGATCCGCATTCGCCCATCGTGGGTGCGCCAGACACACGCCACATGATGAC	40839
Db	4068	CAGCAGATCGCCATATCCGCATCGTGGGTGCGCCAGACACACGCCACATGATGAC	41277
OY	4090	CTGCTGGCCCGCCCATCCAGCCGCGAAGAAAGAGTCTTCAACTCCAGAGAAATTTAGTGG	41499
Db	4128	CTGCTGGCCCGCCCATCCAGCCGCGAAGAAAGAGTCTTCAACTCCAGAGAAATTTAGTGG	41877
OY	4150	CGTCTTAAGAAACGATGACCACTAATTTCTCACCCGATTCMACGTAGACTGACATG	42099
Db	4188	CGTCTTAAGAAACGATGACCACTAATTTCTCACCCGATTCMACGTAGACTGACATG	42477
OY	4210	CGAGCCACAAAGTGTGCTGTGTGTGATACCGTGACCTTTGACCGCCAGGATCCAA	42699
Db	4248	CGAGCCACAAAGTGTGCTGTGTGTGATACCGTGACCTTTGACCGCCAGGATCCAA	43077
OY	4270	TGTCTGAATGTCAAGTATGTGTGACCCCAAGTGTCTCACGTGCTTCCAGCCACTGC	43329
Db	4308	TGTCTGAATGTCAAGTATGTGTGACCCCAAGTGTCTCACGTGCTTCCAGCCACTGC	43677
OY	4330	GGCTTGGCCCTGCTGAATATGCCCACACATTTCAACGAGGCTTCTGCGGTGACAAATGAC	43899
Db	4368	GGCTTGGCCCTGCTGAATATGCCCACACATTTCAACGAGGCTTCTGCGGTGACAAATGAC	44277
OY	4390	TCCCAGAGTCTCCACACCAAGAGGCCACAGACAGCTTGACCTTGAAGGGTGAAG	44499
Db	4428	TCCCAGAGTCTCCACACCAAGAGGCCACAGACAGCTTGACCTTGAAGGGTGAAG	44877
OY	4450	GTGCCAGGAATMACAAACGAGGACGAGAGGCTGGGACAGAGATACATTTGCTCTGAG	45099
Db	4488	GTGCCAGGAATMACAAACGAGGACGAGAGGCTGGGACAGAGATACATTTGCTCTGAG	45477
OY	4510	GAATCAAAAGTCTCATTTATGACAAATGAGCAGAGAGCGTGGACAGAGCCGGTGA	45699
Db	4548	GAATCAAAAGTCTCATTTATGACAAATGAGCAGAGAGCGTGGACAGAGCCGGTGA	46077
OY	4570	GAATTTGAGCTGTGCTTCCGACCGGGATGTATCTATTCATGCTGCCGTTGCTTCC	46229
Db	4608	GAATTTGAGCTGTGCTTCCGACCGGGATGTATCTATTCATGCTGCCGTTGCTTCC	46677
OY	4630	GAATCCGGAATATACAGCCCAAGCA-----	4653
Db	4668	GAATCCGGAATATACAGCCCAAGCAATGTCCCATCATATCGAAGATGAATCTCACCG	47277
OY	4654	-----	4653
Db	4728	CACACCACTGCTGGCCCGGAGAACCTCTAATTGCTAGCTCCAGCTTCCCTGACAA	47877
OY	4654	-----GAAAA	46599
Db	4788	CAGCGCTGGGTACCGCCTTAGAATCAATTTGCGAGGTGGAGAGTTCTAGGAAAA	48477
OY	4660	GCAGAGGTGATGCTCTAACTGCTTGGAACCTCCCGCTGGAACCTGGAAGGTGATGACCT	47179
Db	4848	GCAGAGGTGATGCTCTAACTGCTTGGAACCTCCCGCTGGAACCTGGAAGGTGATGACCT	49077
OY	4720	CTAGACATGAACCTGACCGCTCCCTTCAGTACACAGGTGTGTTGTGTGGACCCGAGAA	47799
Db	4908	CTAGACATGAACCTGACCGCTCCCTTCAGTACACAGGTGTGTTGTGTGGACCCGAGAA	49677
OY	4780	GGGCTCTACGGCTGGAATGTCTTGAAAACTTCCCTAACCCATGTGCCAGAAATTGAGCA	48399
Db	4968	GGGCTCTACGGCTGGAATGTCTTGAAAACTTCCCTAACCCATGTGCCAGAAATTGAGCA	50277
OY	4840	GTCCTTCAAAATTTATATTATCAGAGACCTGGAAGACTACTCATGATAGCAGAGAAAG	48999
Db	5028	GTCCTTCAAAATTTATATTATCAGAGACCTGGAAGACTACTCATGATAGCAGAGAAAG	50877
OY	4900	CGGGCACTGTGTCTTTGTGACGTGAAGAAAGTGAACGTCCCTGGCCCACTCCCACTG	49599
Db	5088	CGGGCACTGTGTCTTTGTGACGTGAAGAAAGTGAACGTCCCTGGCCCACTCCCACTG	51477

QY	4960	CCTGCGCCAGCCCGACATCTTCACCCAACTTTTGAAGTGCAGGGCTGCCATTGT	5013
Db	5148	CCTGCGCCAGCCCGACATCTTCACCCAACTTTTGAAGTGCAGGGCTGCCATTGT	5207
QY	5020	GGGGCAGGCAAGATTGAGAACGGGCTCGCATCTGTGCAAGCATGCCAGCAAGTGC	5079
Db	5208	GGGGCAGGCAAGATTGAGAACGGGCTCGCATCTGTGCAAGCATGCCAGCAAGTGC	5267
QY	5080	ATTCTCCGCTCAACAGAAACCTGACAAATATGCAATCCGGAAAGATAGACCTCA	5139
Db	5268	ATTCTCCGCTCAACAGAAACCTGACAAATATGCAATCCGGAAAGATAGACCTCA	5327
QY	5140	GAGCCCTGCAGCTGATATCACTTACCAATTAACGTAATCTCATTTGGAACCAATAATTC	5199
Db	5328	GAGCCCTGCAGCTGATATCACTTACCAATTAACGTAATCTCATTTGGAACCAATAATTC	5387
QY	5200	TACGAAATCGACATGAAGCAGTACACGCTGAGGAATTCCTCGATTAAGATGACATATCC	5259
Db	5388	TACGAAATCGACATGAAGCAGTACACGCTGAGGAATTCCTCGATTAAGATGACATATCC	5447
QY	5260	TTGGCAGCTGCTGTGTGTTGGCCGCTCTTCCAAACAGTTCCTCTGTCATTCGTGCAAGTG	5319
Db	5448	TTGGCAGCTGCTGTGTGTTGGCCGCTCTTCCAAACAGTTCCTCTGTCATTCGTGCAAGTG	5507
QY	5320	AAACAGCGAGGACAGCGAGAGAGTACTGTGCTGTGTTCCAGATTTGAGATGTCGTG	5379
Db	5508	AAACAGCGAGGACAGCGAGAGAGTACTGTGCTGTGTTCCAGATTTGAGATGTCGTG	5567
QY	5380	GATTCTTAACGGAACCGTAAGCGGACAGACGATCTGTAAGTGCAGTACCTTTGGCC	5439
Db	5568	GATTCTTAACGGAACCGTAAGCGGACAGACGATCTGTAAGTGCAGTACCTTTGGCC	5627
QY	5440	TTTGGCTTACAGAGAACCTTATCTGTGTTGTGACCCACTTCAACTCATCTGAAATTTAG	5499
Db	5628	TTTGGCTTACAGAGAACCTTATCTGTGTTGTGACCCACTTCAACTCATCTGAAATTTAG	5687
QY	5500	ATCCAGGACGCTCTCTGACAGGGAACCTCTGCCAGCGTACTGACATCCGAAACCG	5559
Db	5688	ATCCAGGACGCTCTCTGACAGGGAACCTCTGCCAGCGTACTGACATCCGAAACCG	5747
QY	5560	CGCTAACCTGGGCCCCGTCATTTCTCTGAGAGCGATTAACTTGGGCTCTCATACCAAGAT	5619
Db	5748	CGCTAACCTGGGCCCCGTCATTTCTCTGAGAGCGATTAACTTGGGCTCTCATACCAAGAT	5807
QY	5620	AAATTTAAGGTCATTTGTGTCAGAGGAACCTCGTGAAGAGTCCGSCACTGAACACAC	5679
Db	5808	AAATTTAAGGTCATTTGTGTCAGAGGAACCTCGTGAAGAGTCCGSCACTGAACACAC	5867
QY	5680	CGGGGCCGCTCACCTCCGACAGAGCCCAACAGCGAGGCCCCACCGTACCAAGAG	5739
Db	5868	CGGGGCCGCTCACCTCCGACAGAGCCCAACAGCGAGGCCCCACCGTACCAAGAG	5927
QY	5740	CACATCACCAAGCGGTGGCTTCCAGGCCAGGCGCGCCGAGAGGCCCAACCGCGCA	5799
Db	5928	CACATCACCAAGCGGTGGCTTCCAGGCCAGGCGCGCCGAGAGGCCCAACCGCGCA	5987
QY	5800	GAGCGAAGCAACCCACCGCTAACCGGAGGGGGGAGCCGAGCTGGGCGAGGCAATCT	5859
Db	5988	GAGCGAAGCAACCCACCGCTAACCGGAGGGGGGAGCCGAGCTGGGCGAGGCAATCT	6047
QY	5860	CCTGGCCGCCCTCTGAGCGAGAGTCCCGCGGCGGATGCTTCAAGCAGCGGAGAG	5919
Db	6048	CCTGGCCGCCCTCTGAGCGAGAGTCCCGCGGCGGATGCTTCAAGCAGCGGAGAG	6107
QY	5920	CGGTTCCTCCGGAGAGCTGTTGAAGACAGCAGAGGGGCGGCTGCGGGAGCCGTG	5979
Db	6108	CGGTTCCTCCGGAGAGCTGTTGAAGACAGCAGAGGGGCGGCTGCGGGAGCCGTG	6167
QY	5980	AGGACCCCGCTGCCAGGTGAACAAGGAAGAGGGGAGAGTGCCTCAAGTTTTCAG	6039
Db	6168	AGGACCCCGCTGCCAGGTGAACAAGGAAGAGGGGAGAGTGCCTCAAGTTTTCAG	6227
QY	6040	GTAACTGTACCTATTAT	6060

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Db 6228 AGAAAAACCAACTCTCATCT 6248
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RESULT 8
US-10-028-946-1
; Sequence 1, Application US/10028946
; Publication No. US20020123622A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanhuan
; APPLICANT: Miranda, Maricar
; TITLE OF INVENTION: No. US20020123622A1 Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6165
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-028-946-1

Query Match      86.1%; Score 5661.4; DB 13; Length 6165;
Best local Similarity 95.8%; Pred. No. 0;
Matches 5944; Conservative 0; Mismatches 16; Indels 243; Gaps 3;

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QY 79 GCCAGCGCGGCGCTCCAGGCTGAACTGTTCTTCCAGGAGAAACACCCCTTTATGACTCA 138
Db 61 GCCAGCGCGGCGCTCCAGGCTGAACTGTTCTTCCAGGAGAAACACCCCTTTATGACTCA 120
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QY 199 GAATGAGTCAAGCTGCTCTGATGAAGATTAAAGCAGTGAAGCACTTTGTCGGAATAT 258
Db 181 GAATGAGTCAAGCTGCTCTGATGAAGATTAAAGCAGTGAAGCACTTTGTCGGAATAT 240
QY 259 TCCGACACCATAGCTGAGTTACAGAGCTCCAGCCCTTGCGCAAGGACTTGCAGATCGA 318
Db 241 TCCGACACCATAGCTGAGTTACAGAGCTCCAGCCCTTGCGCAAGGACTTGCAGATCGA 300
QY 319 AGCTCTTGATGTTGCTGCTCACTTTGCTGAAGTGAAGTGTAAAGAGAAACCAACCGAG 378
Db 301 AGCTCTTGATGTTGCTGCTCACTTTGCTGAAGTGAAGTGTAAAGAGAAACCAACCGAG 360
QY 379 GACATCTATAGCTATGAAGTGAAGAAAGGCTTTATTTGGCCCAAGAGCAAGTTTCA 438
Db 361 GACATCTATAGCTATGAAGTGAAGAAAGGCTTTATTTGGCCCAAGAGCAAGTTTCA 420
QY 439 TTTTGTGAGAGAGCGGAAACATATTATCTGAAACACAGCCGCTGATCCCAATTA 498
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QY 1759 CGAGTGAATCTCTACGAATCTGAGAGTCTCGGCTGTCTGTGAAGAAATTCAG 1818
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QY 1819 CGGAAAGCGACAGAAATGTCAGATTAATCTGTTGAAGGCTTAAGATCAAGGAAAGCTGAA 1878
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QY 1879 GTGGGAGAAATATTCGAAACTGAGAAAGATCAATGCTGAGACGAGCTCAAAATTCAGAG 1938
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QY 1939 CTCGAAGAAACTGAGAAAGCT----- 1962
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Db 1921 CTCGAAGAAACTGAGAAAGCTGTAAGAAAGCCAGACGAGGCTGAGCTGCTGAG 1980
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QY 1963 -----GCAAGAGAGCGAGCGGAGGAGCTGAGAGAGCTGCAAGCCGAGAG 2010
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QY 2011 GATTTCTTCTGAGGATCAGAAAGAAAGCTGTGGAAGCTGAGAAAGCGGCTTCTCTG 2070
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QY 2311 AAGAGACACTGAGAGACATGATGACAGAGACAGAGAGAGGCGCATGAGAAAGGCAAA 2370
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QY 2491 CAAAGAACATGAAAGGCGCCAAAGAGATGATTTCTGAATCTCAGGCAACAGAAATTTAC 2550
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QY 2551 CTGGAACACAGGCTGGGAAAGTTGAGAGCCCAAGACCGAAACTGAGAGAGCAGCTGAG 2610
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QY 2731 CTACAGCTCTCCTTGAAGAGCGGAGTCAAGTTGACAGCTTCAAGGCTTGAAGAGGCG 2790
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QY 2911 CTTTCTTAAGCTGTACTGTAAATCAAGACCTGAGAGACAGCTAAACAGGCTGAGCCGAG 2970
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QY 3031 GGCGCCAAAGAGATGTAACCTGCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAG 3090
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Db 3181 TGCACCATGCTGAGAGAACAGGTCATGATTTGAGAGGCTTAAACGATGAGCTGATGAA 3240
| | | | |
QY 3211 AAAAGAGGAGATGAGAGGCTTGAAGAGGCTTCTGGTGAATGAGAAATCCAGTTTGA 3270
| | | | |
Db 3241 AAAAGAGGAGATGAGAGGCTTGAAGAGGCTTCTGGTGAATGAGAAATCCAGTTTGA 3300
| | | | |
QY 3271 TGTGGGTTTGAAGAGCTGAGAGAAATGCTGGAACACCGAAGAAACAGAGAGGCGAGAGCC 3330
| | | | |
Db 3301 TGTGGGTTTGAAGAGCTGAGAGAAATGCTGGAACACCGAAGAAACAGAGAGGCGAGAGCC 3360
| | | | |
QY 3331 GATCAGCGATCAAGAGCTGCGCAGAGTGTGAGAGCTGCGAGTGAAGAGCAAGAGCT 3390
| | | | |
Db 3361 GATCAGCGATCAAGAGCTGCGCAGAGTGTGAGAGCTGCGAGTGAAGAGCAAGAGCT 3420
| | | | |
QY 3391 GAGATTCTGCTCTGAGAGGCTCTCAAGAGCAGAAAGCTGAAGGCGAGAGCTCTCT 3450
| | | | |
Db 3421 GAGATTCTGCTCTGAGAGGCTCTCAAGAGCAGAAAGCTGAAGGCGAGAGCTCTCT 3480
| | | | |
QY 3451 GACAGCTCAATGACTTGAAGAAAGAGCTGCTTAATGCTTGAATGAATGCCGGAAGCTTA 3510
| | | | |
Db 3481 GACAGCTCAATGACTTGAAGAAAGAGCTGCTTAATGCTTGAATGAATGCCGGAAGCTTA 3540
| | | | |
QY 3511 CAGAGAACTGGAAGCTGAAGAGAGCTCAACAGAGGCTTCTGGAAGAGCAAGCCAA 3570
| | | | |
Db 3541 CAGAGAACTGGAAGCTGAAGAGAGCTCAACAGAGGCTTCTGGAAGAGCAAGCCAA 3600
| | | | |
QY 3571 TTAAGAGCAGATGAGCTGAGAAATTAACATTTTCTGCTGCTCAAGAGCTGCA 3630
| | | | |
Db 3601 TTAAGAGCAGATGAGCTGAGAAATTAACATTTTCTGCTGCTCAAGAGCTGCA 3660
| | | | |
QY 3631 GAAAGCTTAAGATCGGCTGATTAATGAAAGACAGAAAGAGCTTGAAGATCAAGCTG 3690
| | | | |
Db 3661 GAAAGCTTAAGATCGGCTGATTAATGAAAGAGAGCTTGAAGATCAAGCTG 3720
| | | | |
QY 3691 GAAACATTCAGATCTTAATCTCATGAAAGAGTGAAGAGGCTTATTTCTCA 3750
| | | | |
Db 3721 GAAACATTCAGATCTTAATCTCATGAAAGAGTGAAGAGGCTTATTTCTCA 3780
| | | | |
QY 3751 CAAACCAAACTCATTTGATTTTCTGAGAGCAAAATGAGCAACTGCTTAAAGAAAG 3810
| | | | |
Db 3781 CAAACCAAACTCATTTGATTTTCTGAGAGCAAAATGAGCAACTGCTTAAAGAAAG 3838
| | | | |
QY 3811 GGTATTATTAATGAGAGAGAAAGAGAGCTGTTTACCAACAGAGCTTCTTGAAGTAC 3870
| | | | |
Db 3839 -----AGGTTCTTGAAGTAC 3855
| | | | |
QY 3871 AATGAGCTGAAGCTGGCCCTGAGAGAGAGAAAGCTCGGTGTCAGAGCTGAAGAGGCT 3930
| | | | |

Db 3856 AATGAGCTGAAGCTGGCCCTGGAGAGAGAAAAGCTCGTGTGCAAGACTGAGGAAGCC 3915
QY 3931 CTTTCAGAAAGACCCGCGATCGAGCTCCGGTCCGCCGGAGAGACTGCCACCGCAAGCA 3990
Db 3916 CTTTCAGAAAGACCCGCGATCGAGCTCCGGTCCGCCGGAGAGACTGCCACCGCAAGCA 3975
QY 3991 ACCGACACCCACACCCATCCAGCGCCAGCGCAAGGAGAGAGATTCGGCAATGTCGCC 4050
Db 3976 ACCGACACCCACACCCATCCAGCGCCAGCGCAAGGAGAGATTCGGCAATGTCGCC 4035
QY 4051 ATGTCGCGGTCCGCAAGACACGACCGCATGATGATGATGATGATGATGATGATGATG 4110
Db 4036 ATGTCGCGGTCCGCAAGACACGACCGCATGATGATGATGATGATGATGATGATGATG 4095
QY 4111 CGAGAGAAAGAGCTTCAACTCCAGAGAAATTTAGTCGCGCTTTAGAGAACGATGAC 4170
Db 4096 CGAGAGAAAGAGCTTCAACTCCAGAGAAATTTAGTCGCGCTTTAGAGAACGATGAC 4155
QY 4171 CACAAATATTCCTACCGGATTCACGTAAGGACTGAATGAGAGCCAAAGTGTGTG 4230
Db 4156 CACAAATATTCCTACCGGATTCACGTAAGGACTGAATGAGAGCCAAAGTGTGTG 4215
QY 4231 TGTCTGATACCGTGCATCTTTGGACCGCAGCATTCGATGATGATGATGATGATGATG 4290
Db 4216 TGTCTGATACCGTGCATCTTTGGACCGCAGCATTCGATGATGATGATGATGATGATG 4275
QY 4291 TGTCAACCCAGAGCTCCAGCGCTTGGCAGCCACTGCGGCTTGTGCTGTGATATG 4350
Db 4276 TGTCAACCCAGAGCTCCAGCGCTTGGCAGCCACTGCGGCTTGTGCTGTGATATG 4335
QY 4351 AACACCTTACCGAGGCTTTCGCGTGCAGAAATGAATCTCCGAGGTCTCCAGAGCAG 4410
Db 4336 AACACCTTACCGAGGCTTTCGCGTGCAGAAATGAATCTCCGAGGTCTCCAGAGCAG 4395
QY 4411 GAGCCGACAGAGCTTGGACCTGGAAGGGTGAATGAGTGCAGAGATTAACAAACGA 4470
Db 4396 GAGCCGACAGAGCTTGGACCTGGAAGGGTGAATGAGTGCAGAGATTAACAAACGA 4455
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QY 4531 GAACAATGAAGCAGAGAGCTGGAAGAGCGCGTGAAGAAATTTAGTGTGCTTCCC 4590
Db 4516 GAACAATGAAGCAGAGAGCTGGAAGAGCGCGTGAAGAAATTTAGTGTGCTTCCC 4575
QY 4591 GACGGGAGATGATTCATTTATGATGTCGTTGCTTCCGAACTCGCAATTAACCCAA 4650
Db 4576 GACGGGAGATGATTCATTTATGATGTCGTTGCTTCCGAACTCGCAATTAACCCAA 4635
QY 4651 GCA----- 4653
Db 4636 GGAAGATGTCCTACTACTACTGAAGATGCAATCTACCGGACACCACTGCTGCCGGG 4695
QY 4654 ----- 4653
Db 4636 AGAACCTCTACTTGTACTAGCTCCAGCTTCCCTGAACAAGCGGTGGGTACACGCTTTA 4755
QY 4654 -----GAAAAAGCAGAGCTGATGCTAACTG 4680
Db 4756 GAATACGTTGTCGAGGTGGAGAGTTCCTAGGAAAAAGCAGAGCTGATGCTAACTG 4815
QY 4681 CTTGGAATCTCCTGCTGAAACTGGAAGGTGATGACCGTCTAGACATGAATGACGCGCTG 4740
Db 4816 CTTGGAATCTCCTGCTGAAACTGGAAGGTGATGACCGTCTAGACATGAATGACGCGCTG 4875
QY 4741 CCCTTCAGTGAACAGGTGTGTTGTGGGACACGAGAGAGGCTCTACGCTCGAATGTC 4800
Db 4876 CCCTTCAGTGAACAGGTGTGTTGTGGGACACGAGAGAGGCTCTACGCTCGAATGTC 4935
QY 4801 TTGAAAACTCCCTTAACCATGTCCTCCAGAAATTTGAGGAGTCTTCAAAATTTATATATTC 4860
Db 4936 TTGAAAACTCCCTTAACCATGTCCTCCAGAAATTTGAGGAGTCTTCAAAATTTATATATTC 4995

QY 4861 AAGACCTGGAAGCTACTCATGATAGCAGAGAGAGCGGGCACTGTGTCTGTGAC 4920
Db 4996 AAGACCTGGAAGCTACTCATGATAGCAGAGAGAGCGGGCACTGTGTCTGTGAC 5055
QY 4921 GTGAAGAAAGTAAACAGTCCCTGGCCAGTCCACCTGCTGCCAGCGGACATCTCA 4980
Db 5056 GTGAAGAAAGTAAACAGTCCCTGGCCAGTCCACCTGCTGCCAGCGGACATCTCA 5115
QY 4981 CCCAATTTTGAAGCTGTCAAGGGCTGCCACTTGTGTTGGGGCAGGCAAGTTAGAAC 5040
Db 5116 CCCAATTTTGAAGCTGTCAAGGGCTGCCACTTGTGTTGGGGCAGGCAAGTTAGAAC 5175
QY 5041 GGGCTTCGATCTGTGACGCAATGCCAGCAAGTGTGATTCCTCGCTACACGAAAC 5100
Db 5176 GGGCTTCGATCTGTGACGCAATGCCAGCAAGTGTGATTCCTCGCTACACGAAAC 5235
QY 5101 CTCAGCAATTAATCTGATCCGAAAGATAGAGACTCAGAGCTCTGACGCTGTATCCAC 5160
Db 5236 CTCAGCAATTAATCTGATCCGAAAGATAGAGACTCAGAGCTCTGACGCTGTATCCAC 5295
QY 5161 TTCACCAATTAACAGTATCTCATTTGGAACCAATTAATCTACGAAATGACATGAAGCAG 5220
Db 5296 TTCACCAATTAACAGTATCTCATTTGGAACCAATTAATCTACGAAATGACATGAAGCAG 5355
QY 5221 TACACGCTGAGAAATTCCTGATTAAGATGACATTCCTTGGCACTGTGTGTTGCC 5280
Db 5356 TACACGCTGAGAAATTCCTGATTAAGATGACATTCCTTGGCACTGTGTGTTGCC 5415
QY 5281 GCTCTTCCAAACAGTTCCCTGTCTCAATTCGTGAGGAGAACAGCGGAGGACAGAG 5340
Db 5416 GCTCTTCCAAACAGTTCCCTGTCTCAATTCGTGAGGAGAACAGCGGAGGACAGAG 5475
QY 5341 GAGTACTTGTGTGTTCCAGAAATTTGAGTGTGTGATTTCTTACGAAAGAGTATG 5400
Db 5476 GAGTACTTGTGTGTTCCAGAAATTTGAGTGTGTGATTTCTTACGAAAGAGTATG 5535
QY 5401 CGCACAGACATCTCAAGTGAATGCTTACTTGTGCTTCTACAGAAACCTGAT 5460
Db 5536 CGCACAGACATCTCAAGTGAATGCTTACTTGTGCTTCTACAGAAACCTGAT 5595
QY 5461 CTGTTTGTGACCCACTTCACTCACTGAAATTAATGATCCAGGACGCTCTCCAGCA 5520
Db 5596 CTGTTTGTGACCCACTTCACTCACTGAAATTAATGATCCAGGACGCTCTCCAGCA 5655
QY 5521 GGAACCCCTGCGGAGGCTACTGGAATCCGGAACCCGCGCTACTTGGGCTTGCAT 5580
Db 5656 GGAACCCCTGCGGAGGCTACTGGAATCCGGAACCCGCGCTACTTGGGCTTGCAT 5715
QY 5581 TCTTCAGAGAGGATTTACTTGGGCTCTCATACAGATTAATTAAGGTGATTTGCTGC 5640
Db 5716 TCTTCAGAGAGGATTTACTTGGGCTCTCATACAGATTAATTAAGGTGATTTGCTGC 5775
QY 5641 AAGGAAACCTCGTGAAGAGATCCGAGACTGAACACCAACGGGAGCCGTCCACTCCGC 5700
Db 5776 AAGGAAACCTCGTGAAGAGATCCGAGACTGAACACCAACGGGAGCCGTCCACTCCGC 5835
QY 5701 AGCAGCCCAACAGAGGAGCCACCAAGTACACAGACATCACCAAGCGGTGGCC 5760
Db 5836 AGCAGCCCAACAGAGGAGCCACCAAGTACACAGACATCACCAAGCGGTGGCC 5895
QY 5761 TCCAGCCCAAGGAGCCGCGGAGGAGCCAGACACCCGAGAGACCAACCCACCGC 5820
Db 5896 TCCAGCCCAAGGAGCCGCGGAGGAGCCAGACACCCGAGAGACCAACCCACCGC 5955
QY 5821 TACCGCAGGAGGAGCAGACGAGCTGCGAGAGACAGTCTCGTGGCGCCCTCTGAGACGA 5880
Db 5956 TACCGCAGGAGGAGCAGACGAGCTGCGAGAGACAGTCTCGTGGCGCCCTCTGAGACGA 6015
QY 5881 GAGAAATTCCTCCGCGGAGTCTCAGACCGCGAGAGAGCGGTCCCGGAGAGCTGTT 5940
Db 6016 GAGAAATTCCTCCGCGGAGTCTCAGACCGCGAGAGAGCGGTCCCGGAGAGCTGTT 6075

QY	6001	AACAAAGGAGAGGAGAGTGC	6023
QY	5941	GAAAGCAGCAGCAGAGGGCCGGCTCC	6000
Db	6076	GAAAGCAGCAGCAGAGGGCCGGCTCC	6135
QY	6136	AACAAAGTCTGGAGCCAGTCTTC	6158

RESULT 9
US-10-79

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: Sequence 1 Application US/10791666
: Publication No. US20040209297A1
: GENERAL INFORMATION:
: APPLICANT: Yu, Xuanchuan
: APPLICANT: Miranda, Maricar
: APPLICANT: Friddele, Carl Johan
: TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
: FILE REFERENCE: LEX-0289-USA
: CURRENT APPLICATION NUMBER: US/10/791,666
: CURRENT FILING DATE: 2004-03-02
: PRIOR APPLICATION NUMBER: US/10/028,946
: PRIOR FILING DATE: 2001-12-20
: PRIOR APPLICATION NUMBER: US 60/258,335
: PRIOR FILING DATE: 2000-12-27.
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 6165
: TYPE: DNA
: ORGANISM: homo sapiens
: US-10-791-666-1

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Query Match	86.1%	Score 5661.4	DB 18	Length 6165
Best Local Similarity	95.8%	Pred. NO. 0		
Matches 5944	Conservative 0	Mismatches 16	Indels 243	Gaps 3

QY	19	ATGTTGAAGTTCAAAATATGAGAGCCGGAAATCCTTTGGATGCTGCTGCTGAACCCATT	78
Db	1	ATGTTGAAGTTCAAAATATGAGAGCCGGAAATCCTTTGGATGCTGCTGCTGAACCCATT	60
QY	79	GCCAGCCGGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACTTTATGACTCA	138
Db	61	GCCAGCCGGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACTTTATGACTCA	120
QY	139	CAGCAGATGTCCTCCTTTCCCGAAGAGGATATAGATGCCCTTTGTTCTCTTTGAA	198
Db	121	CAGCAGATGTCCTCCTTTCCCGAAGAGGATATAGATGCCCTTTGTTCTCTTTGAA	180
QY	199	GAATGACAGTCAGCCGCTCTGATGAAGATTAAAGCAGAGCAACTTTGTCGGAAAGTAT	258
Db	181	GAATGACAGTCAGCCGCTCTGATGAAGATTAAAGCAGAGCAACTTTGTCGGAAAGTAT	240
QY	259	TCCGACACCATAGCTGAGTTACAGAGGCTCCAGCCTTGGCGAAAGAACTTGAAGTCA	318
Db	241	TCCGACACCATAGCTGAGTTACAGAGGCTCCAGCCTTGGCGAAAGAACTTGAAGTCA	300
QY	319	AGCTCTTGAGTTGTGTCTCACTTTGCTGAAGTGCAGTGTGTATGAAGAAAGCAACCGGG	378
Db	301	AGCTCTTGAGTTGTGTCTCACTTTGCTGAAGTGCAGTGTGTATGAAGAAAGCAACCGGG	360
QY	379	GACATCTATGCTATGAAGAAGTGAAGAAAGGCTTATATGGCCACAGACAGGTTTCA	438
Db	361	GACATCTATGCTATGAAGAAGTGAAGAAAGGCTTATATGGCCACAGACAGGTTTCA	420
QY	439	TTTTTTGAGAAGCCGGAACATATTAATCTGAAAGCAAGCCCTGTGATCCCCCAATTA	498
Db	421	TTTTTTGAGAAGCCGGAACATATTAATCTGAAAGCAAGCCCTGTGATCCCCCAATTA	480
QY	499	CAGATGCTTTTCAGAGCAAAAATCACTTTATCTGATGAAGAAATATCAGCTGTGAGGG	558
Db	481	CAGATGCTTTTCAGAGCAAAAATCACTTTATCTGATGAAGAAATATCAGCTGTGAGGG	540

QY	559	GACCTTGCTGTCACTTTTGAATAGATATAGAGACCAAGTTAGATGAATAACCTGTATCAAGTTT	618
Db	541	GACCTTGCTGTCACTTTTGAATAGATAGAGACCAAGTTAGATGAATAACCTGTATCAAGTTT	600
QY	619	TACCTAGCTGAGCTGATTTTGGCTGTTCAAGACGCTTCACTGATGGGATAGCTGATCGA	678
Db	601	TACCTAGCTGAGCTGATTTTGGCTGTTCAAGACGCTTCACTGATGGGATAGCTGATCGA	660
QY	679	GACATCAAGCCTGAGAAACATTCTGTGGACCGCACAGGACACATCAAGCTGGTGGATTTT	738
Db	661	GACATCAAGCCTGAGAAACATTCTGTGGACCGCACAGGACACATCAAGCTGGTGGATTTT	720
QY	739	GGATTCGCCGGGAAATGAATTCAAAACAAATGGTGAATGCCAACTCCCAATTGGGAC	798
Db	721	GGATTCGCCGGGAAATGAATTCAAAACAAATGGTGAATGCCAACTCCCAATTGGGAC	780
QY	799	CCAGATTACATGGCTCCCTGAAGTGTGATCTGTGATGAAACGGGGATGGAAAAAGGACCTAC	858
Db	781	CCAGATTACATGGCTCCCTGAAGTGTGATCTGTGATGAAACGGGGATGGAAAAAGGACCTAC	840
QY	859	GGCCCTGACTGTGACTGTGTGCTCACTGGGCGCTGATTTGCCCTATGAGATGATTTATGGGAGA	918
Db	841	GGCCCTGACTGTGACTGTGTGCTCACTGGGCGCTGATTTGCCCTATGAGATGATTTATGGGAGA	900
QY	919	TCCCCCTTGCAGAGGGAACTCTGCCAANCTTCAATTAACATTATGAAATTTCCAGCGG	978
Db	901	TCCCCCTTGCAGAGGGAACTCTGCCAANCTTCAATTAACATTATGAAATTTCCAGCGG	960
QY	979	TTTTTGAATTTCCAGATGACCCCAAGATGACAGTGACTTTCTTGATCTGATATTCAAAGC	1038
Db	961	TTTTTGAATTTCCAGATGACCCCAAGATGACAGTGACTTTCTTGATCTGATATTCAAAGC	1020
QY	1039	TTGTTGTGCGGCCAGAAAAGAGAGACTGAAGTTTGAAGTCTTTCTCGCATCTTTCTTC	1098
Db	1021	TTGTTGTGCGGCCAGAAAAGAGAGACTGAAGTTTGAAGTCTTTCTCGCATCTTTCTTC	1080
QY	1099	TCTAAATTTGACTGGAACACATCTGTACTCTCTCTCCCTCTGTTCCACCTCTCAAG	1158
Db	1081	TCTAAATTTGACTGGAACACATCTGTACTCTCTCTCCCTCTGTTCCACCTCTCAAG	1140
QY	1159	TCTACAGATGACACTCCCAATTTTGAATGAAACCAAGAAAGAAATTTGGTGGTTCAATCCCT	1218
Db	1141	TCTACAGATGACACTCCCAATTTTGAATGAAACCAAGAAAGAAATTTGGTGGTTCAATCCCT	1200
QY	1219	CGGTGCCAGCTGAGGCCCTCAGGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGGTTTTCG	1278
Db	1201	CGGTGCCAGCTGAGGCCCTCAGGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGGTTTTCG	1260
QY	1279	TACAGCAAGCACTGGGGATTTCTTGATGATCTGATCTGTTGTGTGGGTCTGGAATCC	1338
Db	1261	TACAGCAAGCACTGGGGATTTCTTGATGATCTGATCTGTTGTGTGGGTCTGGAATCC	1320
QY	1339	CCTGCGAAGACTAGCTCCATGGAAGAACTTCTCATCAAAAGCAAAAGACTTCAAGAC	1398
Db	1321	CCTGCGAAGACTAGCTCCATGGAAGAACTTCTCATCAAAAGCAAAAGACTTCAAGAC	1380
QY	1399	TCTCAGGCAAGTGTCAAGATGAGAGGAAATGACCGGTTATCAATCGGAGGTGTCA	1458
Db	1381	TCTCAGGCAAGTGTCAAGATGAGAGGAAATGACCGGTTATCAATCGGAGGTGTCA	1440
QY	1459	GAGGTGAGGCTGTGCTTATGTCAGAGAGGCTGAGCTGAAGGCTCTGACCTCAGAGA	1518
Db	1441	GAGGTGAGGCTGTGCTTATGTCAGAGAGGCTGAGCTGAAGGCTCTGAGACTCAGAGA	1500
QY	1519	TCCCTCTGAGAGCAGACCTTGTACTATCATCAAGATGCAATGCAATGCTTAAAGCAAGT	1578
Db	1501	TCCCTCTGAGAGCAGACCTTGTACTATCATCAAGATGCAATGCAATGCTTAAAGCAAGT	1560
QY	1579	TTGGAGCAAGACCGAATGAGGTGTCCAGAGGATGACAAAGACCTGACGCTTCTCAT	1638
Db	1561	TTGGAGCAAGACCGAATGAGGTGTCCAGAGGATGACAAAGACCTGACGCTTCTCAT	1620
QY	1639	GATATTCAGAGGACAGAGCCGGAAGCTCCAGAAATCAAGAGCAGAGTACAGGCTCA	1698

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Db      1621 GATATCAGAGAGCAGAGCCGGAGAGCTCCAGAAATCAAAGAGAGAGATCCAGGCTCAA 1680
Qy      1699 GTGGAGAAATGAGGTTGATGATGAATCACTGTGGAAAGAGATTTTGTCTCAGCAAGAGA 1758
Db      1681 GTGGAGAAATGAGGTTGATGATGAATCACTGTGGAAAGAGATTTTGTCTCAGCAAGAGA 1740
Qy      1759 CGAGATGATCTCTACGAATCTGAGTGAAGAGTCTCGGCTTGCTGTGAAGAAATTCAG 1818
Db      1741 CGAGATGATCTCTACGAATCTGAGTGAAGAGTCTCGGCTTGCTGTGAAGAAATTCAG 1800
Qy      1819 CGGAAAGCAGACAGATGTGACATTAACCTTTGAAGCTTAAGGATCAAGGAGAGCTTGA 1878
Db      1801 CGGAAAGCAGACAGATGTGACATTAACCTTTGAAGCTTAAGGATCAAGGAGAGAGCTTGA 1860
Qy      1879 GTGGAGAAATGAGGTTGATGATGAATCACTGTGGAAAGAGATTTTGTCTCAGCAAGAGA 1938
Db      1861 GTGGAGAAATGAGGTTGATGATGAATCACTGTGGAAAGAGATTTTGTCTCAGCAAGAGA 1920
Qy      1939 CTCGAGAGAACTGAGAGAGGCT----- 1962
Db      1921 CTCGAGAGAACTGAGAGAGGCTTGAAGAGCAGACCGAGGCCAGAGCTGCTGAG 1980
Qy      1963 -----GCAGAGAGCGAGCCGAGAGGAGCTGAGAGAGCTGAGAACCGAGAG 2010
Db      1981 AATATCCGCGAGGCAAGAGAGCGAGCGAGAGGAGCTGAGAGAGCTGAGAACCGAGAG 2040
Qy      2011 GATTCCTTGAAGAGGCTCAGAAAGAGCTGTGTGAAGCTGAGAGAGCGGCCATTTCTTG 2070
Db      2041 GATTCCTTGAAGAGGCTCAGAAAGAGCTGTGTGAAGAGCTGAGAGAGCGGCCATTTCTTG 2100
Qy      2071 GAGAACAGAGTAAAGAGCTAGAGACCATGAGCGTGAAGAGAAACAGACTGAAGAGTAGC 2130
Db      2101 GAGAACAGAGTAAAGAGCTAGAGACCATGAGCGTGAAGAGAAACAGACTGAAGAGTAGC 2160
Qy      2131 ATCCAGACAAATATCCACAGATCCAGAGATGGCTGATTAATTTCTGAGCTCGAAGAG 2190
Db      2161 ATCCAGACAAATATCCACAGATCCAGAGATGGCTGATTAATTTCTGAGCTCGAAGAG 2220
Qy      2191 AAAACATCGGAGAGGCCCAAGTCTCAGGCCGAGCACTTAGAGTGCATCTGAAACAGAAAG 2250
Db      2221 AAAACATCGGAGAGGCCCAAGTCTCAGGCCGAGCACTTAGAGTGCATCTGAAACAGAAAG 2280
Qy      2251 CAGCATATGAGAGAAAGATTAAGTGTGACAAATCAGATTAAGAGAAACCTGTGCTGAC 2310
Db      2281 CAGCATATGAGAGAAAGATTAAGTGTGACAAATCAGATTAAGAGAAACCTGTGCTGAC 2340
Qy      2311 AAGGAGACCTGAGAGACATGATGCAAGACACGAGAGAGAGGCCCATGAGAGAGGCAAA 2370
Db      2341 AAGGAGACCTGAGAGACATGATGCAAGACACGAGAGAGAGGCCCATGAGAGAGGCAAA 2400
Qy      2371 ATTCTCAGGAAACAGAGGCGATGATCAATGCTATGAGATTCCAAATGCAATCCCTGAA 2430
Db      2401 ATTCTCAGGAAACAGAGGCGATGATCAATGCTATGAGATTCCAAATGCAATCCCTGAA 2460
Qy      2431 CAGAGATTTGTGAACCTGTCTGAAGCAATAAATTGAGCAAAATGAGCTTTTAAAC 2490
Db      2461 CAGAGATTTGTGAACCTGTCTGAAGCAATAAATTGAGCAAAATGAGCTTTTAAAC 2520
Qy      2491 CAAAGAGACATGAGAGGCCCAAGAGAGATGATTTCTGAACTCAGGCAACAGAAATTTTAC 2550
Db      2521 CAAAGAGACATGAGAGGCCCAAGAGAGATGATTTCTGAACTCAGGCAACAGAAATTTTAC 2580
Qy      2551 CTGAGAGACAGAGCTGGAGAGTTGGAGGCCAGAAACCGAAACCTGAGAGAGAGAGCTGAG 2610
Db      2581 CTGAGAGACAGAGCTGGAGAGTTGGAGGCCAGAAACCGAAACCTGAGAGAGAGAGCTGAG 2640
Qy      2611 AAGATCAGGCAACAGACCAAGTGAAGTCAAGATTCGGCTGCTGGAACCTGAGAGCAAGATTG 2670
Db      2641 AAGATCAGGCAACAGACCAAGTGAAGTCAAGATTCGGCTGCTGGAACCTGAGAGCAAGATTG 2700
Qy      2671 CGGAGGTCAGTCTTGAGAGCAGAGAGCAAACTGAGCTCAAGCCGCAAGCTCACAGAG 2730
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Qy      2731 CTACAGCTCTCCCTGAGAGAGCGCAAGTCAAGTTGACAGAGCTTGCAGGCTGCACGGGCG 2790
Db      2761 CTACAGCTCTCCCTGAGAGAGCGCAAGTCAAGTTGACAGAGCTTGCAGGCTGCACGGGCG 2820
Qy      2791 GCCCTGAGAGGACCTTCCGCGAGGAGAGCAGAGCTGAGAGAGACCAAGCAAGAGCT 2850
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Qy      2851 GAAAGAGAGATCAGAGCACTCAGCGCATAGAGTGAATTCAGCGCAAAATTTGATGCT 2910
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Qy      2911 CTTGCTAACAGCTGTACTGTATTCACAGACTGAGAGAGCAGCTTAACCAAGTGCAGAG 2970
Db      2941 CTTGCTAACAGCTGTACTGTATTCACAGACTGAGAGAGCAGCTTAACCAAGTGCAGAG 3000
Qy      2971 GACAAAGCTGAACCTCAACAAACCAAACTTCTACTTGTCCAAACAACTGAGAGGCTTCT 3030
Db      3001 GACAAAGCTGAACCTCAACAAACCAAACTTCTACTTGTCCAAACAACTGAGAGGCTTCT 3060
Qy      3031 GGCAGCAACGACGAGATTTGTAACAATGCAAGTGAAGTGAACATCTCCGCGGAGATC 3090
Db      3061 GGCAGCAACGACGAGATTTGTAACAATGCAAGTGAAGTGAACATCTCCGCGGAGATC 3120
Qy      3091 ACGGAAACGAGATGACAGCTTACAGCCAGAAACCAACAGATGAGGCTTGAACCAACG 3150
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Qy      3151 TGACCATGCTGAGAGAAACAGGTCATGATTTGGAGGCTTAAACGATGAGCTGTAGAA 3210
Db      3181 TGACCATGCTGAGAGAAACAGGTCATGATTTGGAGGCTTAAACGATGAGCTGTAGAA 3240
Qy      3211 AAAGAGCGGAGTGGAGAGGCTTGAAGAGCGTCTCGGCTGATGAAGAAATCCAGTTTGA 3270
Db      3241 AAAGAGCGGAGTGGAGAGGCTTGAAGAGCGTCTCGGCTGATGAAGAAATCCAGTTTGA 3300
Qy      3271 TGTGGGTTGAGAGCTGCAAGAAATGCTGACACCGAGAAACAGAGCGGCGAGAGCC 3330
Db      3301 TGTGGGTTGAGAGCTGCAAGAAATGCTGACACCGAGAAACAGAGCGGCGAGAGCC 3360
Qy      3331 GATCAGCGGATCACCGAGTCTGCGCAAGTGTGAGCTGCGAGTGAAGAGACACAGGCT 3390
Db      3361 GATCAGCGGATCACCGAGTCTGCGCAAGTGTGAGCTGCGAGTGAAGAGACACAGGCT 3420
Qy      3391 GAGATTTCTGCTTGCAGCAGAGCTTCTCAAGAGAGAGGCTGAAGGCCGAGAGCTCTCT 3450
Db      3421 GAGATTTCTGCTTGCAGCAGAGCTTCTCAAGAGAGAGGCTGAAGGCCGAGAGCTCTCT 3480
Qy      3451 GACAAAGCTCAATGACCTGGAAGAGAGATGCTTAATGTAATGCCGGAAGCTTA 3510
Db      3481 GACAAAGCTCAATGACCTGGAAGAGAGATGCTTAATGTAATGCCGGAAGCTTA 3540
Qy      3511 CAGAGAGAGCTGAGAGCTGAACGAGAGCTCAACAGAGGCTTCTGGAAGAGCAAGCCAA 3570
Db      3541 CAGAGAGAGCTGAGAGCTGAACGAGAGCTCAACAGAGGCTTCTGGAAGAGCAAGCCAA 3600
Qy      3571 TTAAGCAGCAGATGAGACTGCAAGAAATCAATTTCCGTCTGACTCAAGAGCTGCA 3630
Db      3601 TTAAGCAGCAGATGAGACTGCAAGAAATCAATTTCCGTCTGACTCAAGAGCTGCA 3660
Qy      3631 GAAAGCTCAGATCGGGCTGATCTACTGAAGCAGAAAGAGTGAAGCTTGAGAGTACAGCTG 3690
Db      3661 GAAAGCTCAGATCGGGCTGATCTACTGAAGCAGAAAGAGTGAAGCTTGAGAGTACAGCTG 3720
Qy      3691 GAAAGCTCAGATCGGGCTGATCTACTGAAGAGAGTGAAGAGTGAAGAGCACTATTTCTCA 3750
Db      3721 GAAAGCTCAGATCGGGCTGATCTACTGAAGAGAGTGAAGAGTGAAGAGCACTATTTCTCA 3780
Qy      3751 CAAACCAAACCTCATTTGATTTTCTGCAAGCCAAATGAGCAACCTGCTTAAGAGAGAG 3810
Db      3781 CAAACCAAACCTCATTTGATTTTCTGCAAGCCAAATGAGCAACCTGCTTAAGAGAGAG - - 3838
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DB 3839 -----AGGTTCTCTGCATGAC 3855
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DB 3916 CTTTCAGAAAGACCCGATTCGAGCTCCGCTCCGCGGAGAGAGCTGCCAAGCAAGCA 3975
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RESULT 10
US-09-964-956-10
; Sequence 10, Application US/09964956
; Publication No. US20040043926A1
; GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Grose, William M
; APPLICANT: Alsodbrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Kerkuda, Ramesh
; APPLICANT: Spletek, Kimberly A
; APPLICANT: Leach, Martin D
; APPLICANT: Shimkels, Richard A
; TITLE OF INVENTION: No. US20040043926A1e1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-124
; CURRENT APPLICATION NUMBER: US/09/964,956
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/235,631
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; PRIOR APPLICATION NUMBER: 60/235,808
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; PRIOR APPLICATION NUMBER: 60/236,065
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; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,399
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,396
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/276,667
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/294,823
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/304,868
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 6189
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-956-10
Query Match      85.7%; Score 5611; DB 11; Length 6189;
Best Local Similarity 95.3%; Pred. No. 0;
Matches 5944; Conservative 0; Mismatches 45; Indels 246; Gaps 4;

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Db 181 GAATCAGTCAAGCTGCTGCTGATGAAGATTAAAGCAGTGAACATTTGTCCGAAAGTAT 240
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| | | | |
QY 4051 ATTCGTCCGTGCGCCAGAGACCAAGCCCATGTGATGAGCTGTGCGCCCGCCATCCAGC 4110
| | | | |
Db 4033 ATTCGTCCGTGCGCCAGAGACCAAGCCCATGTGATGAGCTGTGCGCCCGCCATCCAGC 4092
| | | | |
QY 4111 CGCAGAAAGAGATCTTCAACTCCAGAGAAATTTAGTGGCGTTCTTAAAGAAACGATGAC 4170
| | | | |
Db 4093 CGCAGAAAGAGATCTTCAACTCCAGAGAAATTTAGTGGCGTTCTTAAAGAAACGATGAC 4152
| | | | |
QY 4171 CACAATATTTCTCACCGATTCAACGTAGAGCTGAACATGCGACCAAAAGTGTGTG 4230
| | | | |
Db 4153 CACAATATTTCTCACCGATTCAACGTAGAGCTGAACATGCGACCAAAAGTGTGTG 4212
| | | | |

QY 4231 TGTCTGATACCGTGCATCTTTGACGCCAGGATCCAAATGTCTGAATGTGAGGTGATG 4290
| | | | |
Db 4213 TGTCTGATACCGTGCATCTTTGACGCCAGGATCCAAATGTCTGAATGTGAGGTGATG 4272
| | | | |
QY 4291 TGTCAACCCCAATGCTCCACCGTGTGCGCTTGCAGGACACTGCGGCTTGCCTGAATATGCC 4350
| | | | |
Db 4273 TGTCAACCCCAATGCTCCACCGTGTGCGCTTGCAGGACACTGCGGCTTGCCTGAATATGCC 4332
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QY 4351 ACACATTCACCGAGGCTTCTGCGGTGACAAATGAATCTCCACAGTCTCCAGACCAAG 4410
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Db 4333 ACACATTCACCGAGGCTTCTGCGGTGACAAATGAATCTCCACAGTCTCCAGACCAAG 4392
| | | | |
QY 4411 GAGCCAGAGAGCTTGTGACTTGAAGGCTGATGAAGGTGCCCCAGAAATPACAAACGA 4470
| | | | |
Db 4393 GAGCCAGAGAGCTTGTGACTTGAAGGCTGATGAAGGTGCCCCAGAAATPACAAACGA 4452
| | | | |
QY 4471 GGAACGAAAGCTGGGACAGGAAGTCAATTTGCTGGAGGGATCAAAAGTCTCTAT 4530
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Db 4453 GGAACGAAAGCTGGGACAGGAAGTCAATTTGCTGGAGGGATCAAAAGTCTCTAT 4512
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QY 4531 GACAAATGAAGCCAGAAAGCTGACAGAGCCGCTGGAAGAATTTGAGCTGTGCTTCC 4590
| | | | |
Db 4513 GACAAATGAAGCCAGAAAGCTGACAGAGCCGCTGGAAGAATTTGAGCTGTGCTTCC 4572
| | | | |
QY 4591 GACGGGAAATGATCTATTCATGTGCGCTTGTGTGCTTCCGAATCGCAATPACGCCAA 4650
| | | | |
Db 4573 GACGGGAAATGATCTATTCATGTGCGCTTGTGTGCTTCCGAATCGCAATPACGCCAA 4632
| | | | |
QY 4651 GCA----- 4653
| | | | |
Db 4633 GCAAGTGTCCATATCATCTGAAGATGAATCTGACCCGACACACCTGTGCGCCGG 4692
| | | | |
QY 4654 ----- 4653
| | | | |
Db 4633 AGAAACCTCTACTCTGTAGCTCCAGCTTCCCTGACAAACAGCGCTGAGTACCGCTTA 4752
| | | | |
QY 4654 -----GAAAGCAGAGCTGATGCTAACTG 4680
| | | | |
Db 4753 GAATCATGTTGCGAGGTGGAGAGTTTCTAGGAGAAAGAGAGGCTGATGCTPAACTG 4812
| | | | |
QY 4681 CTTGAAAATCTCCCTGTAATCTGGAAGTGAATGACCGTCTAGACATGAATGACGCTG 4740
| | | | |
Db 4813 CTTGAAAATCTCCCTGTAATCTGGAAGTGAATGACCGTCTAGACATGAATGACGCTG 4872
| | | | |
QY 4741 CCTTCAGTGAACGAGTGTGTTGTGTGGGACCCGAGAGGAGCTCTACCGCTGAATGTC 4800
| | | | |
Db 4873 CCTTCAGTGAACGAGTGTGTTGTGTGGGACCCGAGAGGAGCTCTACCGCTGAATGTC 4932
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QY 4801 TTGAAAAATCTCCCTAACCAATGTCCAGAAATGGAACAGTCTTCAAAATTTATATATC 4860
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QY 4861 AAGGACTTGAAGAACTACTCATGATATGCAAGAGAAAGCGGAGCATGTGTCTTTGAGAC 4920
| | | | |
Db 4993 AAGGACTTGAAGAACTACTCATGATATGCAAGAGAAAGCGGAGCATGTGTCTTTGAGAC 5052
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QY 4921 GTGAAGAAAGTGAACAGTCCCTGAGCCAGTCCCACTGCTGCCAGCCCGACATCTCA 4980
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| | | | |
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QY 5041 GGGCTTGTGATCTGTGAGCCATGCTCCAGAAAGTGTCTATTCTCGCTACAAAGAAAC 5100
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Db 5173 GGGCTTGTGATCTGTGAGCCATGCTCCAGAAAGTGTCTATTCTCGCTACAAAGAAAC 5232
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QY 5101 CTCAGCAAAATPACGATCCGGAAGAAAGATPAGAACTCCAGAGCCGCGAGCTTATCCAC 5160
| | | | |
Db 5233 CTCAGCAAAATPACGATCCGGAAGAAAGATPAGAACTCCAGAGCCGCGAGCTTATCCAC 5292
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QY 5161 TTCAACCAATTAAGTATCTCATTTGAAACCAATPAAATCTACGAAATGACATGAAGAC 5220
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Db      5293  TTACCAATTACAGTATCTTCATTTGAGAACCAATTAATTCACGAATTCAGACGAGAG 5352
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Qy      5281  GCCTTTCCAGAGCTTCCCTGTCTCAATCTGTCAGTGAACGCCAGGCGAGAGAG 5340
Db      5413  GCCTTTCCAGAGCTTCCCTGTCTCAATCTGTCAGTGAACGCCAGGCGAGAGAG 5472
Qy      5341  GAGTACTTCTGTGTTTCCAGAAATTTGAGTGTGTGATTTCTTAACGGAACCTAGC 5400
Db      5473  GAGTACTTCTGTGTTTCCAGAAATTTGAGTGTGTGATTTCTTAACGGAACCTAGC 5532
Qy      5401  CGCAGAGAGATCTCAAGTGAAGTGCCTTACCTTTGACCTTTGCTTACAGAAACCTAT 5460
Db      5533  CGCAGAGAGATCTCAAGTGAAGTGCCTTACCTTTGACCTTTGCTTACAGAAACCTAT 5592
Qy      5461  CTGTTTGTGACCACTTCAATCTGTCAGTGAATTAAGATTCAGGACGCTCTCAGCA 5520
Db      5593  CTGTTTGTGACCACTTCAATCTGTCAGTGAATTAAGATTCAGGACGCTCTCAGCA 5652
Qy      5521  GGGACCCCTGCGGAGCGTACCTGACATCCCGAACCCGCGCTACCTGGCCCTGCATT 5580
Db      5653  GGGACCCCTGCGGAGCGTACCTGACATCCCGAACCCGCGCTACCTGGCCCTGCATT 5712
Qy      5581  TCTCTAGAGAGCAATTAATTTAGGCTCTCTATACAGAGATTAATTAAGGCTATTGCTGC 5640
Db      5713  TCTCTAGAGAGCAATTAATTTAGGCTCTCTATACAGAGATTAATTAAGGCTATTGCTGC 5772
Qy      5641  AAGGAAACCTCTGTGAAGAGTCCGGAATCAACACCGGAGGCGCTTCACTTCCCGC 5700
Db      5773  AAGGAAACCTCTGTGAAGAGTCCGGAATCAACACCGGAGGCGCTTCACTTCCCGC 5832
Qy      5701  AGGAGCCCAACAGAGAGGCGCCAGCCAGCACTCAACAGAGCACTCAACAGGCGTGGCC 5760
Db      5833  AGGAGCCCAACAGAGAGGCGCCAGCCAGCACTCAACAGAGCACTCAACAGGCGTGGCC 5892
Qy      5761  TCCAGCCCAAGCGCGCCCGAGGCGCCAGCCAGCACTCAACAGAGCACTCAACAGGCGT 5820
Db      5893  TCCAGCCCAAGCGCGCCCGAGGCGCCAGCCAGCACTCAACAGAGCACTCAACAGGCGT 5952
Qy      5821  TACCGGAGAGGCGGAGCCAGCTGCGCAGAGGAATTTCTTGGCGCGCGCGCTGGAGCGA 5880
Db      5953  TACCGGAGAGGCGGAGCCAGCTGCGCAGAGGAATTTCTTGGCGCGCGCGCTGGAGCGA 6012
Qy      5881  GAGAAATCCCGCGCGCGAGTGTCAAGACGCGGAGAGAGCGGCTCCCGGAGAGGCTGTTT 5940
Db      6013  GAGAAATCCCGCGCGCGAGTGTCAAGACGCGGAGAGAGCGGCTCCCGGAGAGGCTGTTT 6072
Qy      5941  GAAAGACAGACAGAGGCGCGGCTGCTCGGAGAGCGGTGAGAGACCCCGCTGTCCAGGTG 6000
Db      6073  GAAAGACAGACAGAGGCGCGGCTGCTCGGAGAGCGGTGAGAGACCCCGCTGTCCAGGTG 6132
Qy      6001  AACCAAGGAGAGAGGCGAGATGCTCTCAAGTTTCAAGTTTCACTGTCACTT 6055
Db      6133  AACCAAGGAGAGGCGAGATGCTCTCAAGTTTCAAGTTTCACTGTCACTT 6187

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RESULT 11

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US-10-262-511-1
; Sequence 1, Application US/10262511
; Publication No. US2004003823A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millett, Isabelle
; APPLICANT: Beyman, John A.
; APPLICANT: Kexuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Paturajan, Meera

```

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; APPLICANT: Spylek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Elberman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zeirhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Caterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkels, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Bergins, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT FILING DATE: 2003-05-28
; PRIOR FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuroSeqList version 0.1
; SEQ ID NO 1
; LENGTH: 6189
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(6159)
US-10-262-511-1
Query Match      85.7%; Score 5631; DB 17; Length 6189;
Best Local Similarity 95.3%; Pred. No. 0;
Matches 5944; Conservative 0; Mismatches 45; Indels 246; Gaps 4;

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Qy      19  ATGTGGAAGTTCAATATATGAGCGCGGAATCTTTGAGATGCTGTGCTGCTGAACCCATT 78
Db      1  ATGTGGAAGTTCAATATATGAGCGCGGAATCTTTGAGATGCTGTGCTGCTGAACCCATT 60
Qy      79  GCCAGCGGCGCTCCAGGCTGAATCTGTCTTCCAGGGAACCAACCCCTTTATGACTCA 138
Db      61  GCCAGCGGCGCTCCAGGCTGAATCTGTCTTCCAGGGAACCAACCCCTTTATGACTCA 120
Qy      139  CAGCAGATGCTCTCTTTTCCGAGAGAGGATATTAGATGCCCTTTGTTCTTTTGA 198
Db      121  CAGCAGATGCTCTCTTTTCCGAGAGAGGATATTAGATGCCCTTTGTTCTTTTGA 180

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QY 199 GAATGCAGTCAAGCTGCTGTGATGAAGTTTAAGCAAGTGAACAATTGTCCTGGAAATAT 258
DB 181 GAATGCAGTCAAGCTGCTGTGATGAAGTTTAAGCAAGTGAACAATTGTCCTGGAAATAT 240
QY 259 TCCGACACCAATAGCTGAGTTACAGAGCTCCAGCTTCGGCAAAAGACTTCGAAGTCAGA 318
DB 241 TCCGACACCAATAGCTGAGTTACAGAGCTCCAGCTTCGGCAAAAGACTTCGAAGTCAGA 300
QY 319 AGCTTGTAGTGTGTGTCACTTGTCTGAAGTGCAGGTGTAAAGAGAAAGCAACCGAG 378
DB 301 AGCTTGTAGTGTGTGTCACTTGTCTGAAGTGCAGGTGTAAAGAGAAAGCAACCGAG 360
QY 379 GACATCTATGCTATGAAGTGAAGAGAAAGAGCTTTATGGCCCAAGAGGTTTCA 438
DB 361 GACATCTATGCTATGAAGTGAAGAGAAAGAGCTTTATGGCCCAAGAGGTTTCA 420
QY 439 TTTTGTGAGAGAGAGCGGAAATATATCTCGAAGCAAGCCCGTGTATCCCCCAATTA 498
DB 421 TTTTGTGAGAGAGAGCGGAAATATATCTCGAAGCAAGCCCGTGTATCCCCCAATTA 480
QY 499 CAGATGCTCTTTCAGGACAAATAATCACTTTATCTGATGAGAGAAATATCAAGCTTGAAG 558
DB 481 CAGATGCTCTTTCAGGACAAATAATCACTTTATCTGATGAGAGAAATATCAAGCTTGAAG 540
QY 559 GACTTGCTGTCACTTTTGAATAGATAGAGACCAAGTTAGATGAATAAAGCTGATACGTTT 618
DB 541 GACTTGCTGTCACTTTTGAATAGATAGAGACCAAGTTAGATGAATAAAGCTGATACGTTT 600
QY 619 TACCTGCTGAGCTGATTTTGGCTGTTCACAGCTTCATCTGATGGGATACGTGATCGA 678
DB 601 TACCTGCTGAGCTGATTTTGGCTGTTCACAGCTTCATCTGATGGGATACGTGATCGA 660
QY 679 GACATCAAGCTGAGAGACATTCGTGACCGCAGAGACACATCAAGCGTGGATTTT 738
DB 661 GACATCAAGCTGAGAGACATTCGTGACCGCAGAGACACATCAAGCGTGGATTTT 720
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QY 1039 TTGTTGTGCGGCGCAAGAAAGAGACTGAATTTGAAGTCTTTGCTGCAATCTTTCTTC 1098
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QY 1099 TCTAAATTTGATGAGAAACAATTGTGAATCTCTCTCCCTCTGTTCCACCTCTCAAG 1158
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QY 1159 TCTGACGATGACACTCCCAATTTTGTATGAACCAAGAGAAATGCTGGGTTTCAATCCCT 1218
DB 1138 TCTGACGATGACACTCCCAATTTTGTATGAACCAAGAGAAATGCTGGGTTTCAATCCCT 1197
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DB 1318 CCGTGCAGCTGAGGCTCTCAAGCTTCTCGGCTGAAGAACTGCGTGTGTGGGTTTTTCG 1377
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DB 1378 TCTCAGGACAAAGTGTCAACAAGATGAGAGGAAATGACCCGGTTTCACTGAGAGTGTCA 1437
QY 1459 GAGGTGAGAGCTGTGCTTACTGATGAAGAGGTTGAGCTGAAGGCTCTGAGACTGAGGA 1518
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QY 1519 TCCCTCTGAGAGCAGACCTTGTCTACTCAATCAAGAAATGATGATGTTAAAGGAAAT 1578
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QY 1699 GTGGAAGAAATGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1758
DB 1678 GTGGAAGAAATGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1737
QY 1759 CCGAGTGTCTCTACGAATCTGAGCTGAGAGAGTCTGGCTTGTCTGAAAGAAATTCAG 1818
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DB 1798 CGAAAGGACAGAGATGTCAACATTAACCTGTTGAAGCTTAAGATCAAGGGAAGCTCGAA 1857
QY 1879 GTGGAAGAAATGCGAAACTGGAAGAGATCAATGCTGAGCAGCACTGCAAAATTCAGAG 1938
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QY 1939 CTCGAAGAGAACTGGAAGAGCTG----- 1963
DB 1918 CTCGAAGAGAACTGGAAGAGCTGTAAGAACCAAGCAGCAGAGGCTGCTGCAAG 1977
QY 1964 -----CAAGGACGAGCCGAGAGGAGCTGGAAGAGCTGCAAGAACCGAGAG 2010
DB 1978 AATATCCGCAAGGCAAGAGGAGCCGAGAGGAGCTGGAAGAGCTGCAAGAACCGAGAG 2037
QY 2011 GATTTCTTCTGAAGGCTCAAGAAAGAGCTGTGGAAGCTGAGGAACGCGCCATTTCTCTG 2070
DB 2038 GATTTCTTCTGAAGGCTCAAGAAAGAGCTGTGGAAGCTGAGGAACGCGCCATTTCTCTG 2097
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QY 2311 AAGGAGCACTGAGAGAACTGATCAGAGACAGAGAGAGGCTCATGAGAGAGGCAAA 2370

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Qy 2371 ATTCTCAGCGAACAAGAGCGATGATCAATGCTATGATTCCAAAGATCAGATCCCTGGAA 2430
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Qy 2491 CAAAGAACATGAAAGGCCCAAGAAAGATGATTTCTGAACTCAGGCAACAGAAATTTTAC 2550
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Qy 2611 AAGATCAGCCACCAAGACCAAGTGAACAAGATCGGCTGCGAACTGAGACAAAGATTG 2670
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Qy 2971 GACAAAGCTGAATCTCAACAAACAAAATTCTACTTGTCCAAACAACTCGATGAGGCTTC 3030
Db 2998 GACAAAGCTGAATCTCAACAAACAAAATTCTACTTGTCCAAACAACTCGATGAGGCTTC 3057
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Qy 3211 AAAAGACGAGAGTGGAGAGGCTTGGAGAGGCTCTGGGTGATGAGAAATCCAGTTTGA 3270
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Db 3298 TGTGGGTTTGAAGAGCTGACAGAGATGCTGACACCGAAGAACAGAGCGGGGAGAGCC 3357
Qy 3331 GATCAGCGATCACCGAGTCTGCGCAGGCTGAGAGCTGAGAGTGAAGAGCAAGAGCT 3390
Db 3358 GATCAGCGATCACCGAGTCTGCGCAGGCTGAGAGCTGAGAGTGAAGAGCAAGAGCT 3417
Qy 3391 GAGATTCTGCTCTGACAGAGGCTCTCAAAGACAGAAAGCTGAAGGCGGAGAGCTCTCT 3450
Db 3418 GAGATTCTGCTCTGACAGAGGCTCTCAAAGACAGAAAGCTGAAGGCGGAGAGCTCTCTCT 3477

Qy 3451 GAAAGCTCAATGACCTTGGAGAAAGAGATGCTATGCTTGAATGAAATGCCGAAGCTTA 3510
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Db 3538 CAGCAAGAGCTGAGAGCTGAGAGAGAGCTCAACAGAGGCTTCTGGAGAGCAAGCCAAA 3597
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Qy 3811 GGTATATTAGTGAACGAAAGAGACCTGCTTACCAACAGGCTCTGACAGTAC 3870
Db 3836 -----AGGTGCTCTGACAGTAC 3852
Qy 3871 AATGAGCTGAGAGCTGAGCCCTGAGAGAAAGAGTCTGCTGACAGAGTGAAGAGCC 3930
Db 3893 AATGAGCTGAGAGCTGAGCCCTGAGAGAAAGAGTCTGCTGACAGAGTGAAGAGCC 3912
Qy 3931 CTTTCAAGAACCCGCAATGAGCTCCGCTCCGCGGAGAGAGCTGCCACCGCAAGCA 3990
Db 3913 CTTTCAAGAACCCGCAATGAGCTCCGCTCCGCGGAGAGAGCTGCCACCGCAAGCA 3972
Qy 3991 ACAGAACCAACCAACCCATGCAAGCAGGCAACGAGGAGCAGAGATGCGCATGTCCGC 4050
Db 3973 ACAGAACCAACCAACCCATGCAAGCAGGCAACGAGGAGCAGAGATGCGCATGTCCGC 4032
Qy 4051 ATCTGTCGCTGCGCAGAGACCAAGCCAGTGCATGAGCTGAGCCCGGCATTCAGC 4110
Db 4033 ATCTGTCGCTGCGCAGAGACCAAGCCAGTGCATGAGCTGAGCCCGGCATTCAGC 4092
Qy 4111 CCGAGAAAGAGTCTTCAATCTCAGAGAAATTTAGTCCGCTCTTAAGGACGATGCAC 4170
Db 4093 CCGAGAAAGAGTCTTCAATCTCAGAGAAATTTAGTCCGCTCTTAAGGACGATGCAC 4152
Qy 4171 CAACAATTTCTCAACGATTTCAACGTAAGGACTGAACATGCGAGCCACAAGGTGCTGTC 4230
Db 4153 CAACAATTTCTCAACGATTTCAACGTAAGGACTGAACATGCGAGCCACAAGGTGCTGTC 4212
Qy 4231 TGTCTGATACCGTGTGACTTGAAGCCAGGATCCAAATGTCTGAAATGTGAGTGATG 4290
Db 4213 TGTCTGATACCGTGTGACTTGAAGCCAGGATCCAAATGTCTGAAATGTGAGTGATG 4272
Qy 4291 TGTCAACCCCAAGTGTCTCAAGTCTTGCAGCCCACTGCGGCTGCTGCTGATATGCC 4350
Db 4273 TGTCAACCCCAAGTGTCTCAAGTCTTGCAGCCCACTGCGGCTGCTGCTGATATGCC 4332
Qy 4351 ACAACCTTCAACGAGGCTTCTGCGGTGCAAAATGAAATCTCCCAAGGTCTCAGAACCA 4410
Db 4333 ACAACCTTCAACGAGGCTTCTGCGGTGCAAAATGAAATCTCCCAAGGTCTCAGAACCA 4392
Qy 4411 GAGCCAGAGAGAGTGTGCACTTGAAGAGGTGATGAAGTCCAGAAATTAACAAACGA 4470
Db 4393 GAGCCAGAGAGAGTGTGCACTTGAAGAGGTGATGAAGTCCAGAAATTAACAAACGA 4452
Qy 4471 GGAACGAAGGCTGGAGACAGAAATGATGATGCTGAGAGGATCAAAAGTCTCATTTAT 4530
Db 4453 GGAACGAAGGCTGGAGACAGAAATGATGATGCTGAGAGGATCAAAAGTCTCATTTAT 4512

QY	4531	GACAAATGAAGCCAGAGAAACCTGGCAGAGCCGGGTGGAAAGAAATTTGAGCTGTGCTTCCC	4550
Db	4513	GACATGAAGCCAGAAACCTGAGCAGAGCCGGTGGAAAGAAATTTGAGCTGTGCTTCCC	4572
QY	4591	GACGGGGATGTATTCTATTGATGGTCCGTTGGTGTCTCGAACTCGCAAAATACAGCCAA	4650
Db	4573	GACGGGGATGTATTCTATTGATGGTCCGTTGGTGTCTCGAACTCGCAAAATACAGCCAA	4632
QY	4651	GCA-----	4653
Db	4633	GCAGATGTCCCATACATACTAAGATGGAATCTCACCCGCAACCACTGTGGCCCGG	4692
QY	4654	-----	4653
Db	4693	AGAACCTCTACTGTGTGCTGCTCCAGCTTCCCTGCAAAACAGCGTGGGTACCGCCTTA	4752
QY	4654	-----GAAAAAGCAAGACTGATGCTAAACTG	4680
Db	4753	GAATCAGTTTGCCAGGTGGAGAGATTTCTAGGGAAAAAGCAAGACTGATGCTAAACTG	4812
QY	4681	CTTGGAAATCTCCCTGTGTGAACTGGAAGGTATATGACCGTCTAGACATGAACTGACGCTG	4740
Db	4813	CTTGGAAATCTCCCTGTGTGAACTGGAAGGTATATGACCGTCTAGACATGAACTGACGCTG	4872
QY	4741	CCCTTCAGTACCAAGTGGTGTGGTGGGACCCGAGAAAGGCTCTACGCGCTGAATGTC	4800
Db	4873	CCCTTCAGTACCAAGTGGTGTGGTGGGACCCGAGAAAGGCTCTACGCGCTGAATGTC	4932
QY	4801	TTGAAAACTCCCTTAAACCATGTCCCAAGAAATTTGAGAGATCTTCCAAATTTATATATC	4860
Db	4933	TTGAAAACTCCCTTAAACCATGTCCCAAGAAATTTGAGAGATCTTCCAAATTTATATATC	4992
QY	4861	AAGACCTGGAAGACTACTGATGATACAGAGAAAGACCGGAGCATGTGTCTTGTGGAC	4920
Db	4993	AAGACCTGGAAGACTACTGATGATACAGSTGAAGCGGGCATGTGTCTTGTGGAC	5052
QY	4921	GTGAAGAAAGTGAACACTCCCTGGCCCAATGCCACTGTGCTGCCAGCCCGACATCTCA	4980
Db	5053	GTGAAGAAAGTGAACACTCCCTGGCCCAATGCCACTGTGCTGCCAGCCCGACATCTCA	5112
QY	4981	CCCAACATTTTGAAGCTGTCAAGGGCTGCACATTGTTGGGGCAGGCAAGATTGAGAAC	5040
Db	5113	CCCAACATTTTGAAGCTGTCAAGGGCTGCACATTGTTGGGGCAGGCAAGATTGAGAAC	5172
QY	5041	GGGCTCTGCAATCTGTGACGCCATGCCACAGCAAAATGCTCATTTCTCGCTACCAAGAAAC	5100
Db	5173	GGGCTCTGCAATCTGTGACGCCATGCCACAGCAAAATGCTCATTTCTCGCTACCAAGAAAC	5232
QY	5101	CTCAGCAAAATCTGCATCCGGAAGAGATGAGACCTCAGAGCCCTGCACTGTATCTCC	5160
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QY	5161	TTCAACCAATTAACGATATCTCATTTGGAACCAATAAATTTTACAGAAATCGACATGAAGCAG	5220
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QY	5221	TACAGCGCTCGAGGAATTCGGAATAAGAACCAATTCCTTTGCACTGTGTGTGTTGCC	5280
Db	5353	TACAGCGCTCGAGGAATTCGGAATAAGAACCAATTCCTTTGCACTGTGTGTGTTGCC	5412
QY	5281	GCTCTTTCGAACAGCTTCCCTGTCTCAATCGTGACGGTGAACCGCAGCGGACGACGAG	5340
Db	5413	GCTCTTTCGAACAGCTTCCCTGTCTCAATCGTGAGGTGAACCGCAGCGGACGACGAG	5472
QY	5341	GAGTACTTGTCTGTGTTTCCAGAAATTTGGAGTGTTCGTGGATTTCTTACGGAAGCGTATC	5400
Db	5473	GAGTACTTGTCTGTGTTTCCAGAAATTTGGAGTGTTCGTGGATTTCTTACGGAAGCGTATC	5532
QY	5401	CGCACAAGCATCTCAAGTGAAGTGCCTTACCTTTGGCCTTTGACAGAGAAACCTTAT	5460
Db	5533	CGCACAAGCATCTCAAGTGAAGTGCCTTACCTTTGGCCTTTGACAGAGAAACCTTAT	5592
QY	5461	CTGTGTTGTGACCACTTCAACTCACTCGAAGTAATGATTCAGGCAACGCTTCTCAGCA	5520

Db 5593 CTGTTGTGTACCCACTTCAACTCACTCGAAGTAATTGAGATCCAGGACGCTCTCAGCA 5652

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Db 5653 GGGACCCCTGCGCCGAGCGTACCTGGACATCCGGAACCCGCGCTACTGGGCGCTCGCANT 5712

Qy 5581 TCTCTGAGCGATTTACTTGGCGTCTCTCATACAGAGTAATTAAGGCTATTGGCTGC 5640

Db 5713 TCTCTGAGCGATTTACTTGGCGTCTCTCATACAGAGTAATTAAGGCTATTGGCTGC 5772

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Db 5773 AAGGGAAACCTGTGAAGAGTCCGGCACTGAACACACCGGGGCGCTCCACTTCCGC 5832

Qy 5701 AGCAGCCCCCAACAGCGAGCCCAACCCAGTACCAACGAGCATCAACCAAGCGCTGGCC 5760

Db 5833 AGCAGCCCCCAACAGCGAGCCCAACCCAGTACCAACGAGCATCAACCAAGCGCTGGCC 5892

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Db 5893 TCCAGCCCAAGCGCGCCCGGAGAGGCCCAACCCAGCCACCCGCGAGCCACACCCACCGC 5952

Qy 5821 TACCCGAGAGGGCGGAGCCGAGCTGCGAGGGGACAAGTCTCGGCGCGCCCTCGAGGGA 5880

Db 5953 TACCCGAGAGGGCGGAGCCGAGCTGCGAGGGGACAAGTCTCGGCGCGCCCTCGAGGGA 6012

Qy 5881 GAGAGTCTCCCGCGCGATGCTCAGACGCGGAGAGACCGTCCCGGAGGCTGT 5940

Db 6013 GAGAGTCTCCCGCGCGATGCTCAGACGCGGAGAGACCGTCCCGGAGGCTGT 6072

Qy 5941 GAAAGCAGCAGAGGGGCGCGCTGCGGGGAGCCGTAAGAGACCCGCTTCCAGGTG 6000

Db 6073 GAAAGCAGCAGAGGGGCGCGCTGCGGGGAGCCGTAAGAGACCCGCTTCCAGGTG 6132

Qy 6001 AACAAAGGAGAGGGCAGAGTGCCTCTCAAGTTTCAAGTTTAACTGTCACTGCACT 6055

Db 6133 AACAAAGTGTGGAGCAAGTCTTCAAGTAAATTCAGCAGAGAAAACCAACTCT 6187

RESULT 12

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/ TITLE OF INVENTION: No. US20040043926A1 Proteins and Nucleic Acids Encoding Same

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PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 127
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 6201
TYPE: DNA
ORGANISM: Homo sapiens
US-09-964-956-8

Query Match 85.6%; Score 5629.8; DB 11; Length 6201;
Best Local Similarity 95.7%; Pred. No. 0;
Matches 5929; Conservative 0; Mismatches 22; Indels 246; Gaps 4;

19 ATGTTAAAGTTCAAAATATGAGCGCGGAATCTTTGGATGCTGCTGTGAACCAT 78
1 AGTTTAAAGTTCAAAATATGAGCGCGGAATCTTTGGATGCTGCTGTGAACCAT 60
79 GCAGCGCGGCGCTCCAGGCGTGAATCTGTTCTCCAGGGGAAACACCCCTTATGACTCA 138
61 GCGAGCGGCGCTCCAGGCGTGAATCTGTTCTCCAGGGGAAACACCCCTTATGACTCA 120
139 CAGCAGATGCTCTCTCTCTCCGAGAAAGGATATTAAGTCCCTCTTGTCTCTTGA 198
121 CAGCAGATGCTCTCTCTCCGAGAAAGGATATTAAGTCCCTCTTGTCTCTTGA 180
199 GAATGAGTCAAGCTGCTGATGAAGATTAAAGCAGTGAACCTTTGTCGGAAGTAT 258
181 GAATGAGTCAAGCTGCTGATGAAGATTAAAGCAGTGAACCTTTGTCGGAAGTAT 240
259 TCCGACACCATAGCTAGTTAGAGAGCTCCAGCTTCGCAAGGATTCGAAATCAGA 318
241 TCCGACACCATAGCTAGTTAGAGAGCTTCAGCTTCGCAAGGATTCGAAATCAGA 300
319 AGCTCTGAGTGTGCTCACTTGTGCTGAAGTGCAGGTGCTAAGAGAAAGCAACCGG 378
301 AGCTCTGAGTGTGCTCACTTGTGCTGAAGTGCAGGTGCTAAGAGAAAGCAACCGG 360
379 GACATCTATGCTATGAAGTATGAAGAGAGGCTTTATTTGGCCAGAGCAGTTTCA 438
361 GACATCTATGCTATGAAGTATGAAGAGAGGCTTTATTTGGCCAGAGCAGTTTCA 420
439 TTTTGAAGAAAGGGAACATATTAATCTCGAAGCAAGCCCGTGAATCCCAATTA 498
421 TTTTGAAGAAAGGGAACATATTAATCTCGAAGCAAGCCCGTGAATCCCAATTA 480
499 CAGTATGCTTTGAGCAAAATATCACTTTATCTGATGAGAGAAATATCAGCTGAGG 558
481 CAGTATGCTTTGAGCAAAATATCACTTTATCTGATGAGAGAAATATCAGCTGAGG 540
559 GACTTCTGTCACTTTGATATGATATGAGAGCAGTTAGATGAATAAAGCTGATACAGTT 618
541 GACTTCTGTCACTTTGATATGATATGAGAGCAGTTAGATGAATAAAGCTGATACAGTT 600
619 TACCTAGCTGAGCTGATTTTGGCTGTTCAAGGCTTCATGATGGATCGTGCATCGA 678

601 TACCTAGCTGAGCTGATTTTGGCTGTTCAAGGCTTCATCTGATGGATACGTCATCGG 660
679 GACATCAAGCTGAGAAACATTTCTGTTGACCCGACAGGACATCAAGTGTGATTTT 738
661 GACATCAAGCTGAGAAACATTTCTGTTGACCCGACAGGACATCAAGTGTGATTTT 720
739 GATCTGCGCGGAAATGAATCAACAGATGTGAATGCCAACTCCGATTTGGGACC 798
721 GATCTGCGCGGAAATGAATCAACAGATGTGAATGCCAACTCCGATTTGGGACC 777
799 CCAGATTACATGCTCTCTGAAGTGTGATGATGAAGCGGATGAGAAAGCACTTAC 858
778 CCAGATTACATGCTCTCTGAAGTGTGATGATGAAGCGGATGAGAAAGCACTTAC 837
859 GGCCTGAGCTGTGATCTGTGTGATGATGAGGCGGTGATTTGATGATGATTTATGGAGA 918
838 GGCCTGAGCTGTGATCTGTGTGATGATGAGGCGGTGATTTGATGATGATTTATGGAGA 897
919 TCCCGCTTGCAGAGGGAACCTCTGCGAGAACCTTCAATTAATTAATTAATTCAGCG 978
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1378 TCTCAGAGCAAGTGTCAAAAGTGAAGAGCAAGCAAGCTTACATCTGAGAGTGTCA 1437
1459 GAGGTGAGAGCTGTGTTAGTGAAGAGAGTGAAGTGAAGGCTCTGAGAGTGTCA 1518
1438 GAGGTGAGAGCTGTGTTAGTGAAGAGAGTGAAGTGAAGGCTCTGAGAGTGTCA 1497
1519 TCCCTCTGAGAGAGAGCTTGTCTACCTCATCAAGATGAGAGTGAAGTGAAGGCT 1578
1498 TCCCTCTGAGAGAGAGCTTGTCTACCTCATCAAGATGAGAGTGAAGTGAAGGCT 1557
1579 TTGAGCAAGCAAGATGAGAGTGTCCAGAGAGTGAAGCAAGCAAGCTTCTCAT 1638
1558 TTGAGCAAGCAAGATGAGAGTGTCCAGAGAGTGAAGCAAGCAAGCTTCTCAT 1617
1639 GATATCAGAGCAAGAGCCGGAAGCTTCCAGAGAGTGAAGCAAGCAAGCTTCTCAT 1698
1618 GATATCAGAGCAAGAGCCGGAAGCTTCCAGAGAGTGAAGCAAGCAAGCTTCTCAT 1677
1699 GTGAGAGAAATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1758

Db 1678 GTGGAAGAAATGAGTTGATGTAATCACTTGGAAAGGATCTTGTCTCAGCAAGAGA 1737
QY 1759 CGAGTGAATCTCTACGAATCTGAGCTGAGAGACTCTCGGCTTGTCTCTGAAGATTCAAG 1818
Db 1738 CGAGAGATCTCTACGAATCTGAGCTGAGAGACTCTCGGCTTGTCTCTGAAGATTCAAG 1797
QY 1819 CGGAAGCGACAGAAATGTGACATAAAGTTGAAGCTTAAGATCAAGGGAAGGCTGAA 1878
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Db 1858 GTGGAGAAATATGCGAACTGAGAGATCAATGCTGAGCAGAGCTCAAAATTCAGAG 1917
QY 1939 CTCCAGAGAAACTGAGAAAGGCT----- 1962
Db 1918 CTCCAGAGAAACTGAGAAAGGCTGTAAAGCCAGACGAGGCGCACCGAGCTGCTGAG 1977
QY 1963 -----GCAAGAGCGAGCGCGAGAGGAGCTGGAAGAGCTGAGAACCGAGAG 2010
Db 1978 AATATCCGCGACAGCAAGAGAGCGCGAGAGGAGCTGGAAGAGCTGAGAACCGAGAG 2037
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Db 2038 GATTTCTTGAAGGATCAGAAAGAAAGCTGTGGAAGCTGAGAAAGCGCGCAATTCCTG 2097
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Db 2098 GAGAACAAAGGTAAAGACTAAGAACATGAGACCTGAGAAAGAAACAGACTGAAGATGAC 2157
QY 2131 ATCCAGACAAAATCCCAAGATCCAGAGATGAGCTGATAAATTTGAGCTCGAAGAG 2190
Db 2158 ATCCAGACAAAATCCCAAGATCCAGAGATGAGCTGATAAATTTGAGCTCGAAGAG 2217
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Db 2518 CAAAGGAACATGAAGGCCCAAGAAAGATGATTTCTGAATCTCAGGCAACAGAAATTTTAC 2577
QY 2551 CTGAGACACAGAGCTGGAAAGTTGAGGCCCAAGAACGAAATCTGAGAGAGAGCTGAG 2610
Db 2578 CTGAGACACAGAGCTGGAAAGTTGAGGCCCAAGAACGAAATCTGAGAGAGAGCTGAG 2637
QY 2611 AAGATCAGCACCAAGACACAGAGTGCAGGAATCGGCTGTGGAATCTGAGACAGAGATTG 2670
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QY 2671 CGGAGAGTCAATCTAGAGACAGAGACAGAAACTGAGACTCAAGCGCAGCTCACAG 2730
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QY 2731 CTACAGCTCTCCTGTGAGAGAGCGGAGTCAAGTTGACAGCCTGTGAGGCTGACGAGGCG 2790
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QY 2791 GCCCTGAGAGCGCAAGCTTCCGAGCGGAAGACAGAGCTGGAAGAGACCAACAGAGAGCT 2850
Db 2818 GCCCTGAGAGCGCAAGCTTCCGAGCGGAAGACAGAGCTGGAAGAGACCAACAGAGAGCT 2877
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QY 3031 GGCAGCAACGAGAGATTTATACAACTGAGAGTGAAGTGAACCATCTCGCGGAGAGATC 3090
Db 3058 GGCAGCAACGAGAGATTTATACAACTGAGAGTGAAGTGAACCATCTCGCGGAGAGATC 3117
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QY 3511 CAGCAAGAGCTGAGAGCTGAACAGAGAGCTCAACAGAGGCTTTGGAAGAGCAAGCCAAA 3570
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3991 ACGGACCAACCCCAATCCAGCGAGCCACCGGAGGAGAGAGATCCGCATGTCCGCC 4050
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4171 CACAAATATTTCTTCAACCGATTCAGAGCTGAGACATGAGCCCAAAAGTGTCTGTG 4230
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US-10-262-511-13
; Sequence 13, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Yu, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojie (Sasha)
; APPLICANT: Patlurajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyanar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Carterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: Cureseqblast version 0.1
; SEQ ID NO 13

; LENGTH: 6201
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(6198)
US-10-262-511-13
Query Match 85.6%; Score 5629.8; DB 17; Length 6201;
Best Local Similarity 95.7%; Pred. No. 0;
Matches 5929; Conservative 0; Mismatches 22; Indels 246; Gaps 4;
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QY 4471 GGCACGAAAGCTGGACAGAAAGTACATGTCTGAGAGGATCAAAAATGCTCATTTAT 4530
| | | | |
Db 4453 GGCACGAAAGCTGGACAGAAAGTACATGTCTGAGAGGATCAAAAATGCTCATTTAT 4512
| | | | |
QY 4531 GACAAATGAAGCCAGAGAAAGCTGGAACAGAGCCGCTGGAAGAAATTTGAGCTGCTTCC 4590
| | | | |
Db 4513 GACAAATGAAGCCAGAGAAAGCTGGAACAGAGCCGCTGGAAGAAATTTGAGCTGCTTCC 4572
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QY 4591 GACGGGATGTATCATTTCAATGTGCGTGTGCTTCCGAACTCGCAAAATACAGCCAA 4650
| | | | |
Db 4573 GACGGGATGTATCATTTCAATGTGCGTGTGCTTCCGAACTCGCAAAATACAGCCAA 4632
| | | | |
QY 4651 GCA----- 4653
| | | | |
Db 4633 GCAAGATGCCCATACATACGAAAGATGAATCTCACCCGACACACCTGTGCGCGG 4692
| | | | |
QY 4654 ----- 4653
| | | | |
Db 4633 AGAACCTCTACTTGTCTAGCTCCAGCTTCCCTGACAAACAGCGTGGTCAACGCTTA 4752
| | | | |
QY 4654 -----GAAAAAGCAGAAAGCTGATGCTTAACTG 4680
| | | | |
Db 4753 GAATCAGTTGTCGAGGTGGAGAGTTTCTAGGAAAAAGCAGAGCTGATGCTTAACTG 4812
| | | | |
QY 4681 CTTGAAAAATCCCTGCTGAAACTGAAAGTGTATGACCTGTAACATGAACCTGACGCTG 4740
| | | | |
Db 4813 CTTGAAAAATCCCTGCTGAAACTGAAAGTGTATGACCTGTAACATGAACCTGACGCTG 4872
| | | | |
QY 4741 CCTTCAGTGAACAGGT 4800
| | | | |
Db 4873 CCTTCAGTGAACAGGT 4932
| | | | |
QY 4801 TTGAAAAATCTCCCTAACCCATGTCCAGAAATGAGCACTTCCAAATTTATATTATC 4860
| | | | |
Db 4933 TTGAAAAATCTCCCTAACCCATGTCCAGAAATGAGCACTTCCAAATTTATATTATC 4992
| | | | |
QY 4861 AAGGACCTGGAAGAGCTACATGATATGAGAGAAAGAGGGGACCTGTGTCTTGTGAC 4920
| | | | |
Db 4993 AAGGACCTGGAAGAGCTACATGATATGAGAGAAAGAGGGGACCTGTGTCTTGTGAC 5052
| | | | |
QY 4921 GTGAGAAAGTGAAGAGCTCCCTGAGCCAGTCCCACTGTGCTCCAGCCGACATCTCA 4980
| | | | |
Db 5053 GTGAGAAAGTGAAGAGCTCCCTGAGCCAGTCCCACTGTGCTCCAGCCGACATCTCA 5112
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QY 4981 CCCAATTTTGTGAAGTGTCAAGGCTGCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5040
| | | | |
Db 5113 CCCAATTTTGTGAAGTGTCAAGGCTGCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5172
| | | | |
QY 5041 GGGCTGCACTGTGTGACAGCATGCCCAGCAAGTGTGATTTCTGCTTACAAAGCAAAAC 5100
| | | | |
Db 5173 GGGCTGCACTGTGTGACAGCATGCCCAGCAAGTGTGATTTCTGCTTACAAAGCAAAAC 5232
| | | | |
QY 5101 CTCAGCAAAATCTGATCCGAGAAAGATAGAGACTTCAGAGCCCTGAGCTGTATCCAC 5160
| | | | |

5233 CTCAGCAATATCTGCAATCCGGAAAGATGAGACCTCAGAGCCCTGCACTGATATCCAC 5292
5161 TTCACCAATTAAGATATCTCATTTGAGAACCAATTAATTTACGAAATCGACATGAACAG 5220
5293 TTCACCAATTAAGATATCTCATTTGAGAACCAATTAATTTACGAAATCGACATGAACAG 5352
5221 TACAGCCTGAGGAATTTCTGATTAAGATGACATTTCTTGACACTGTGTGTGGC 5280
5353 TACAGCCTGAGGAATTTCTGATTAAGATGACATTTCTTGACACTGTGTGTGGC 5412
5281 GCCTTTCCAAAGCTTTCCCTGCTCAATGTGACAGTGAACAGCGACGAGGACGAGAG 5340
5413 GCCTTTCCAAAGCTTTCCCTGCTCAATGTGACAGTGAACAGCGACGAGGACGAGAG 5472
5341 GAGTACTGCTGTGTTCACGAAATTTGAGTTCGTGATTTCTTACGGAAGACGTAGC 5400
5473 GAGTACTGCTGTGTTCACGAAATTTGAGTTCGTGATTTCTTACGGAAGACGTAGC 5532
5401 CGGACGAGATCTCAAGTGAATCGCTTACCTTTGGCCTTTGGCCTTACAGAAACCTTAT 5460
5533 CGGACGAGATCTCAAGTGAATCGCTTACCTTTGGCCTTTGGCCTTACAGAAACCTTAT 5592
5461 CTGTTTGTGACCACTTCAACTCACTGAAATTAATTAATTAATTAATTAATTAATTAAT 5520
5593 CTGTTTGTGACCACTTCAACTCACTGAAATTAATTAATTAATTAATTAATTAATTAAT 5652
5521 GGGACCCCTGCGGACGCTACCTGACATCCCGACCCGCTACCTGGGCTCTGCAT 5580
5653 GGGACCCCTGCGGACGCTACCTGACATCCCGACCCGCTACCTGGGCTCTGCAT 5712
5581 TCTCTGAGAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5640
5713 TCTCTGAGAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5772
5641 AAGGAAACCTCGTGAAGAGTCCGGCACTGAACCAACCGGAGCCCGTCCACCTCCGC 5700
5773 AAGGAAACCTCGTGAAGAGTCCGGCACTGAACCAACCGGAGCCCGTCCACCTCCGC 5832
5701 AAGGAAACCTCGTGAAGAGTCCGGCACTGAACCAACCGGAGCCCGTCCACCTCCGC 5760
5833 AAGGAAACCTCGTGAAGAGTCCGGCACTGAACCAACCGGAGCCCGTCCACCTCCGC 5892
5761 TCCAGCCCAAGCCCGCCGAGGAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAG 5820
5893 TCCAGCCCAAGCCCGCCGAGGAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAG 5952
5821 TACCGGAGGAGGAGGAGCCGAGCTGCGGAGGAGCAAGCTCTGCGGAGCCCGTGAAGCGA 5880
5953 TACCGGAGGAGGAGGAGCCGAGCTGCGGAGGAGCAAGCTCTGCGGAGCCCGTGAAGCGA 6012
5881 GAGAAATCTCCCGCCGCGATGCTCAAGCAAGCGAGAGAGCGATCCCGGAGGAGCTGTT 5940
6013 GAGAAATCTCCCGCCGCGATGCTCAAGCAAGCGAGAGAGCGATCCCGGAGGAGCTGTT 6072
5941 GAGAAATCTCCCGCCGCGATGCTCAAGCAAGCGAGAGAGCGATCCCGGAGGAGCTGTT 6000
6073 GAGAAATCTCCCGCCGCGATGCTCAAGCAAGCGAGAGAGCGATCCCGGAGGAGCTGTT 6132
6001 AACCAAGGAGAGGAGCA 6017
6133 AACCAAGGAGAGGAGCA 6149

RESULT 14

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; GENERAL INFORMATION:

; APPLICANT: Yu, Xuanchuan

; APPLICANT: Mirand, Maricar

; APPLICANT: Fridde, Carl Johan

; TITLE OF INVENTION: No. US20020123622A1el Human Kinases and Polynucleotides Encoding

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; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 5877
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-028-946-3

Query Match 81.5%; Score 5358; DB 13; Length 5877;

Best Local Similarity 95.8%; Pred. No. 0; Matches 5634; Conservative 0; Mismatches 5; Indels 243; Gaps 3;

19 ATGTTGAAGTTCAATATGAGACCGCGAATCTTTGATGCTGCTGCTGAACCAT 78
1 ATGTTGAAGTTCAATATGAGACCGCGAATCTTTGATGCTGCTGCTGAACCAT 60
79 GCGAGCCGGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACACCTTTATGACTCA 138
61 GCGAGCCGGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACACCTTTATGACTCA 120
139 GCGAGATGCTCTCTCTTTCCGAGAGGGATTAATAGATGCTGCTGCTTTGTA 198
121 GCGAGATGCTCTCTCTTTCCGAGAGGGATTAATAGATGCTGCTGCTTTGTA 180
199 GAATGAGTCAAGCTGCTGCTGATGAAGATTAAGACGTGAGCAATTTGTCGGAAT 258
181 GAATGAGTCAAGCTGCTGCTGATGAAGATTAAGACGTGAGCAATTTGTCGGAAT 240
259 TCCGACCAATAGCTGATTAAGAGCTCCAGCTTCGCAAGAGACTTCCAGATCA 318
241 TCCGACCAATAGCTGATTAAGAGCTCCAGCTTCGCAAGAGACTTCCAGATCA 300
319 AGCTTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 378
301 AGCTTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
379 GACATCTATGCTATGAAATGATGAAGAGAGCTTTATTTGAGCCGAGAGAGCTTTCA 438
361 GACATCTATGCTATGAAATGATGAAGAGAGCTTTATTTGAGCCGAGAGAGCTTTCA 420
439 TTTTGTGAGAAAGAGGAAATATTTATCTGAAGCAAGCCCGTGAATCCCAATTA 498
421 TTTTGTGAGAAAGAGGAAATATTTATCTGAAGCAAGCCCGTGAATCCCAATTA 480
499 CAGTATGCTTTCAAGACAAATATCACTTTATCTGAAGCAAGCCCGTGAAGAGG 558
481 CAGTATGCTTTCAAGACAAATATCACTTTATCTGAAGCAAGCCCGTGAAGAGG 540
559 GACTTCTGCTACTTTTGAATAGATGAAGACCAAGTATGATGAAGAACTGATACAGTT 618
541 GACTTCTGCTACTTTTGAATAGATGAAGACCAAGTATGATGAAGAACTGATACAGTT 600
619 TACCTAGCTGAGCTGATTTTGGCTGTTCAAGGCTTCATCTGATGAGATACGATCGA 678
601 TACCTAGCTGAGCTGATTTTGGCTGTTCAAGGCTTCATCTGATGAGATACGATCGA 660
679 GACATCAAGCTGAGAAACATTTCTGCTGACCCGACAGGACATCACTCAAGGCTGATTT 738
661 GACATCAAGCTGAGAAACATTTCTGCTGACCCGACAGGACATCACTCAAGGCTGATTT 720
739 GATCTGCGCGGAAATGAATTAACAAGATGATGATGCAAACTCCGATTTGGAGC 798
721 GATCTGCGCGGAAATGAATTAACAAGATGATGATGCAAACTCCGATTTGGAGC 780
799 CAGATTAATGAGCTCTGATGATGCTGATGATGATGATGATGATGATGATGATGATGAT 858
781 CAGATTAATGAGCTCTGATGATGCTGATGATGATGATGATGATGATGATGATGATGAT 840

QY	859	GGCTGAGACGTGTA	CTGTGTGTGT	CAGTGTGGGCTGTAGTTGCTTATGATGATTTATGGAGAG	918
Db	841	GGCTTGACCTGTAC	CTGGTGTGT	CAGTGTGGGCTGTATGCTTATGATGATTTATGGAGAG	900
QY	919	TTCCCTCTGCGACAGAGGA	ACTCTGTGCAGAACCTTCAATTAACATTAATTAATTAACAGCG	978	
Db	901	TTCCCTCTGCGACAGAGGA	ACTCTGTGCAGAACCTTCAATTAACATTAATTAATTAATTAACAGCG	960	
QY	979	TTTTTGAATTTTCAAGTGA	CCCCCAAAAGTGAAGTGA	CTTCTTGAATCTGAATTCAAAGC	103
Db	961	TTTTTGAATTTTCAAGTGA	CCCCCAAAAGTGAAGTGA	CTTCTTGAATCTGAATTCAAAGC	102
QY	1039	TTGTTGTGGGGCCAGAAAGAGAGAC	TGAAGTTTGAAGGTCTTGTGCGCAATCCTTCTTC	109	
Db	1021	TTGTTGTGGGGCCAGAAAGAGAGAC	TGAAGTTTGAAGGTCTTGTGCGCAATCCTTCTTC	108	
QY	1099	TTCTAAATTTGACTGGAACCA	ATTCTGTAACTCTCTCTCCCTCCCTGCTTCCCACTTCAAG	115	
Db	1081	TTCTAAATTTGACTGGAACCA	ATTCTGTAACTCTCTCTCCCTCCCTGCTTCCCACTTCAAG	114	
QY	1159	TTCTGACGATGACACCTCCCAATTTT	TGATGAACCGAAGAAATTCGTGGGTTTCACTCTCT	121	
Db	1141	TTCTGACGATGACACCTCCCAATTTT	TGATGAACCGAAGAAATTCGTGGGTTTCACTCTCT	120	
QY	1219	CCGTGCGACCTGAGCCCTCAGGCTT	CTCGGGTGAAGAACTGCGCTTGTGGGGTTTTCG	127	
Db	1201	CCGTGCGACCTGAGCCCTCAGGCTT	CTCGGGTGAAGAACTGCGCTTGTGGGGTTTTCG	126	
QY	1279	TACAGGAAGGCACTGGGGATTC	TGGTGAATCTGAATCTGTTGTGTGTGTCGGGTCTGCACTCC	133	
Db	1261	TACAGGAAGGCACTGGGGATTC	TGGTGAATCTGAATCTGTTGTGTGTGTCGGGTCTGCACTCC	132	
QY	1339	CCTGCCAAGACTAGCTCCATGTGA	AAAAAGAACTTCTCATCAAAAGCAAAAGACTACAGAC	139	
Db	1321	CCTGCCAAGACTAGCTCCATGTGA	AAAAAGAACTTCTCATCAAAAGCAAAAGACTACAGAC	138	
QY	1399	TCTCAGGACAACTGTTCACAAAT	TGAGACGAGAAATGACCCGGTTACATCGAAGAGTGTCA	145	
Db	1381	TCTCAGGACAACTGTTCACAAAT	TGAGACGAGAAATGACCCGGTTACATCGAAGAGTGTCA	144	
QY	1459	GAGGTGAGGCTGTGCTTAGT	CAGAAAGAGGTGTGAAGCTTGAAGGCTCTGAGACTGACAGA	151	
Db	1441	GAGGTGAGGCTGTGCTTAGT	CAGAAAGAGGTGTGAAGCTTGAAGGCTCTGAGACTGACAGA	150	
QY	1519	TTCCCTCTGAGACAGAGACTTGTCT	ACTTCACTACAGAAATGCAATGACATTAAGCGAAGT	157	
Db	1501	TTCCCTCTGAGACAGAGACTTGTCT	ACTTCACTACAGAAATGCAATGACATTAAGCGAAGT	156	
QY	1579	TTTGAAGCAAGACGAGTGA	AGGTGTCCACAGAGATGACAAAGCACTGAGGTTTCCAT	163	
Db	1561	TTTGAAGCAAGACGAGTGA	AGGTGTCCACAGAGATGACAAAGCACTGAGGTTTCCAT	162	
QY	1639	GATATCAAGAGACAGAGCCGGA	AGCTCCAGAAATCAAAAGACAGAGATCCAGGCTCA	169	
Db	1621	GATATCAAGAGACAGAGCCGGA	AGCTCCAGAAATCAAAAGACAGAGATCCAGGCTCA	168	
QY	1699	GTGGAAGAAATGAGGTTGAT	GTATGTGAATGAAAGAGATCTTGTCTCAGCAAGAGA	175	
Db	1681	GTGGAAGAAATGAGGTTGAT	GTATGTGAATGAAAGAGATCTTGTCTCAGCAAGAGA	174	
QY	1759	CGAGATGATCTTCAAGAA	CTTGAGCTGAGAGAGTCTCGGCTTGTGCTGAAGAAATTCAG	181	
Db	1741	CGAGATGATCTTCAAGAA	CTTGAGCTGAGAGAGTCTCGGCTTGTGCTGAAGAAATTCAG	180	
QY	1819	CGGAAAGCGACAGAAATG	TCACATTAACCTGTTGAAGGCTTAAGATCAAGGGAAGCTTGA	187	
Db	1801	CGGAAAGCGACAGAAATG	TCACATTAACCTGTTGAAGGCTTAAGATCAAGGGAAGCTTGA	186	
QY	1879	GTGGAGAAATATGCGAAA	CTGAGAGAGATCAATGTCTGACGACAGACTCAAAATTCAGAG	193	
Db	1861	GTGGAGAAATATGCGAAA	CTGAGAGAGATCAATGTCTGACGACAGACTCAAAATTCAGAG	192	
QY	1939	CTCCAAGAGAACTGAGAGAGCT	-----	1962	

Db	1921	CTCCAGAGAAACTGGAGAAAGGCTGTAAAGCCAGACGAGGCCACCGAGCTGCTGAC	1981
Qy	1963	-----GCAAAGAGGAGACCCGAGAGGAGCTGTGAGAAAGCTGTCAAACTCGAGAG	2011
Db	1981	AATATCCGCACGACAAAGAGGAGCGACCCGAGAGGAGCTGTGAAACCTGTCAAGAACCGAGAG	2041
Qy	2011	GAATCTTCTGAAGGCATCAGAAAGAAGCTGTGTGAAGCTGTGAGAACGCGCCCATCTCTGTG	2070
Db	2041	GAATCTTCTGAAGGCATCAGAAAGAAGCTGTGTGAAGCTGTGAGAACGCGCCCATCTCTGTG	2100
Qy	2071	GAGAACCAAGTTAAAGACTTAGAGCAATGTGAGCTTAGAAGAACAGACTGAGAGTAGAC	2130
Db	2101	GAGAACCAAGTTAAAGACTTAGAGCAATGTGAGCTTAGAAGAACAGACTGAGAGTAGAC	2160
Qy	2131	ATCCAGACAAATCCCAACAGATCCAGAGATGTGTGATTAATTTCTGAGAGTCGAGAG	2190
Db	2161	ATCCAGACAAATCCCAACAGATCCAGAGATGTGTGATTAATTTCTGAGAGTCGAGAG	2220
Qy	2191	AAACATCCGGAGGCCCAAGTCTCAGCCGACGACTTAGAAGTGCACCTTGAAAACAGAAAGAG	2250
Db	2221	AAACATCCGGAGGCCCAAGTCTCAGCCGACGACTTAGAAGTGCACCTTGAAAACAGAAAGAG	2280
Qy	2251	CAGCACTATGAGGAAAGAATTAAGTGTGAGCAATCGATTAAGAAAGACCTGTGCAC	2310
Db	2281	CAGCACTATGAGGAAAGAATTAAGTGTGAGCAATCGATTAAGAAAGACCTGTGCAC	2340
Qy	2311	AAGAGACACTGTGAGAACATATATGACAGACACGAGAGAGGCCCATGAGAGGGCAAA	2370
Db	2341	AAGAGACACTGTGAGAACATATATGACAGACACGAGAGAGGCCCATGAGAGGGCAAA	2400
Qy	2371	ATTCTCAGCGAAACGAAAGGCGATATCAATGCTATGATTTCCAGATCATGATTCCTGTGA	2430
Db	2401	ATTCTCAGCGAAACGAAAGGCGATATCAATGCTATGATTTCCAGATCATGATTCCTGTGA	2460
Qy	2431	CAGAGGATTTGTGAACCTGTCTGAAGCCCAATTAACCTTGACGCAAAATAGCAGCTTTTACC	2490
Db	2461	CAGAGGATTTGTGAACCTGTCTGAAGCCCAATTAACCTTGAGCAAAATAGCAGCTTTTACC	2520
Qy	2491	CAAGAGAACATGAAAGGCCCAAGAGATGATTTCTGAATCTCAGGCAACAGAAATTTTAC	2550
Db	2521	CAAGAGAACATGAAAGGCCCAAGAGATGATTTCTGAATCTCAGGCAACAGAAATTTTAC	2580
Qy	2551	CTGGAACAACAGGCTGGGAAGTTGTGAGGCCCAAGCCGAAAATCTGAGAGCAGCTGGAG	2610
Db	2581	CTGGAACAACAGGCTGGGAAGTTGTGAGGCCCAAGCCGAAAATCTGAGAGCAGCTGGAG	2640
Qy	2611	AAAGATCAAGCCCAACAAACACATGTCACAAAGATGTGCTGTGGAATCTGTAGACAAAGTTG	2670
Db	2641	AAAGATCAAGCCCAACAAACACATGTCACAAAGATGTGCTGTGGAATCTGTAGACAAAGTTG	2700
Qy	2671	CGGAGAGGTCAGTCTAGAGACAGAGGACAGAAACTGAGCTCAAGCGCCAGCTCACAGAG	2730
Db	2701	CGGAGAGGTCAGTCTAGAGACAGAGGACAGAAACTGAGCTCAAGCGCCAGCTCACAGAG	2760
Qy	2731	CTAACAAGCTTCTCTGTGACGAGCGCGAGTCAACAGTTGACAGCCCTTGACGAGCTGACCGGCG	2790
Db	2761	CTAACAAGCTTCTCTGTGACGAGCGCGAGTCAACAGTTGACAGCCCTTGACGAGCTGACCGGCG	2820
Qy	2791	GCCCTGTGAGAGCCAGCTTGCGCAGCGCGAACAACAGCTGTGAAGAGACACAGGAGAAAGCT	2850
Db	2821	GCCCTGTGAGAGCCAGCTTGCGCAGCGCGAACAACAGCTGTGAAGAGACACAGGAGAAAGCT	2880
Qy	2851	GAAAGAGAGATCCAGGCACTCACGGCACATAGAGATGAATTCAGCGCAAAATTTGATGCT	2910
Db	2881	GAAAGAGAGATCCAGGCACTCACGGCACATAGAGATGAATTCAGCGCAAAATTTGATGCT	2940
Qy	2911	CTTCGTAAACAGCTGTACTGTAAATCAACAGACTGTGAGAGAGAGAGCTTAATCCAGCTGACCGAG	2970
Db	2941	CTTCGTAAACAGCTGTACTGTAAATCAACAGACTGTGAGAGAGAGAGCTTAATCCAGCTGACCGAG	3000
Qy	2971	GACAAACGCTTAATCAACAAACAAATCTTACTTGTCCAAACAATCTGATGAGGCTTCT	3030

Db 3001 GACAAAGCTGAACTCAACAAACAACTTCTACTTGTCCAAACAACTGATGAGGCTCT 3060
Qy 3031 GGGGCCAAGCAAGATTTGTAACAATGCGAAAGTGAATGCATCTCCGCCGGGAGATC 3090
Db 3061 GGGGCCAAGCAAGATTTGTAACAATGCGAAAGTGAATGCATCTCCGCCGGGAGATC 3120
Qy 3091 ACCGAAAGAGATGAGCTTACAGCAGAGCAAAACATGAGAGGCTCTGAGACACAG 3150
Db 3121 ACCGAAAGAGATGAGCTTACAGCAGAGCAAAACATGAGAGGCTCTGAGACACAG 3180
Qy 3151 TGCACCATGCTGAGAGAAACAGTCAATGATTTGAGAGCCCTTAAACGATGAGCTGTAAG 3210
Db 3181 TGCACCATGCTGAGAGAAACAGTCAATGATTTGAGAGCCCTTAAACGATGAGCTGTAAG 3240
Qy 3211 AAAAGACGCGAGTGGAGAGGCTCTGAGAGAGGCTCTGGGTGATGAGAAATCCAGTTTGA 3270
Db 3241 AAAAGACGCGAGTGGAGAGGCTCTGAGAGAGGCTCTGGGTGATGAGAAATCCAGTTTGA 3300
Qy 3271 TGTGGGGTTGAGAGCTGAGAGAAATGCTGGAACCGAGAAACAGAGCAGGGGAGAGCC 3330
Db 3301 TGTGGGGTTGAGAGCTGAGAGAAATGCTGGAACCGAGAAACAGAGCAGGGGAGAGCC 3360
Qy 3331 GATCAGCGATCAACCGAGTCTCGCAGGTGAGTGAAGCTGAGTGAAGACAAAGGCT 3390
Db 3361 GATCAGCGATCAACCGAGTCTCGCAGGTGAGTGAAGCTGAGTGAAGACAAAGGCT 3420
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Db 3421 GAGATTCTGCTCTGACAGAGGCTCTCAAAAGACAGAGCTGAAGGCGGAGGCTCTCT 3480
Qy 3451 GACAACTCAATGACCTGAGAGAAAGACATGATGTTGAATGAATGCGCGAGCTTA 3510
Db 3481 GACAACTCAATGACCTGAGAGAAAGACATGATGTTGAATGAATGCGCGAGCTTA 3540
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Qy 3571 TTAACAGCAGATGAGCTGCAAGAAATCAATTTCCGTCTGACTCAAGACTGCA 3630
Db 3601 TTAACAGCAGATGAGCTGCAAGAAATCAATTTCCGTCTGACTCAAGACTGCA 3660
Qy 3631 GAAAGCTGATGAGGCTGACTACTGAGAGACAGAAAGAAAGTGAATGAGTACGAG 3690
Db 3661 GAAAGCTGATGAGGCTGACTACTGAGAGACAGAAAGAAAGTGAATGAGTACGAG 3720
Qy 3691 GAAACATTCAGGTTCTATTTCTCATGAAAGTGAAGTGAAGGCACTATTTCTCA 3750
Db 3721 GAAACATTCAGGTTCTATTTCTCATGAAAGTGAAGTGAAGGCACTATTTCTCA 3780
Qy 3751 CAAACCAAACTCATTTATTTCTGCAAGCCAAATGACCAACTGCTAAAAAGAAA 3810
Db 3781 CAAACCAAACTCATTTATTTCTGCAAGCCAAATGACCAACTGCTAAAAAGAAA 3838
Qy 3811 GGTATTATTAGTGAAGGAAAGAACCCCTTTAACCAACAGGTTCTCTGCACTAC 3870
Db 3839 -----AGGTTCTCTGCACTAC 3855
Qy 3871 AATGAGCTGAGCTGAGCCCTGAGAGAGAGAAAGCTCGCTGTCAGAGCTTGAAGAGCC 3930
Db 3856 AATGAGCTGAGAGCTGAGCCCTGAGAGAGAGAAAGCTCGCTGTCAGAGCTTGAAGAGCC 3915
Qy 3931 CTTTCAAGAGACCGCATGAGCTCCGGTCCGCCGGAGAGAGCTGCCCAAGCAAGCA 3990
Db 3916 CTTTCAAGAGACCGCATGAGCTCCGGTCCGCCGGAGAGAGAGCTGCCCAAGCAAGCA 3975
Qy 3991 AGGAGCAACCCCAACCATCAAGCCAGCCACCGCAGAGGAGAGATCCGATGCTCCGC 4050
Db 3976 AGGAGCAACCCCAACCATCAAGCCAGCCACCGCAGAGGAGAGATCCGATGCTCCGC 4035
Qy 4051 ATGCTGCGGTGCGCAGAGCAACGAGCCAGTGCATGAGCTGTGGCCCGGCATCCAGC 4110
Db 4036 ATGCTGCGGTGCGCAGAGCAACGAGCCAGTGCATGAGCTGTGGCCCGGCATCCAGC 4095

Qy 4111 CGAGAGAGAGGCTTCAACTCCAGAGGAAATTTAGTGGGCTTTAAGGAACGATGCAC 4170
Db 4096 CGAGAGAGAGGCTTCAACTCCAGAGGAAATTTAGTGGGCTTTAAGGAACGATGCAC 4155
Qy 4171 CACAATATTTCTCAACCGATTCAACGTAGAGCTGAACATGCGAGCCCAAAAGTGTGCTG 4230
Db 4156 CACAATATTTCTCAACCGATTCAACGTAGAGCTGAACATGCGAGCCCAAAAGTGTGCTG 4215
Qy 4231 TGTCTGGAATCCGTGACCTTTGAGAGCCAGGCAATCCAAATGCTCGAATGTCAGTGA 4290
Db 4216 TGTCTGGAATCCGTGACCTTTGAGAGCCAGGCAATCCAAATGCTCGAATGTCAGTGA 4275
Qy 4291 TGTCAACCCCAAGTGCACAGTGTGCTGCGAGGCACTGAGGCTGCTGCTGAATATGCG 4350
Db 4276 TGTCAACCCCAAGTGCACAGTGTGCTGCGAGGCACTGAGGCTGCTGCTGAATATGCG 4335
Qy 4351 ACACATTCACCGAGGCTTCTGCGGTGACAAATGAACTCCCGAGGTCTCCAGACCAAG 4410
Db 4336 ACACATTCACCGAGGCTTCTGCGGTGACAAATGAACTCCCGAGGTCTCCAGACCAAG 4395
Qy 4411 GAGCCAGACAGAGCTTGCACCTGGAAGGTGATGAGTGCAGAAATTAACAACGA 4470
Db 4396 GAGCCAGACAGAGCTTGCACCTGGAAGGTGATGAGTGCAGAAATTAACAACGA 4455
Qy 4471 GGAACGAGAGCTGGAGACAGAAAGTCAATTTGCTGAGAGGATCAAAAGTCCATTTAT 4530
Db 4456 GGAACGAGAGCTGGAGACAGAAAGTCAATTTGCTGAGAGGATCAAAAGTCCATTTAT 4515
Qy 4531 GACAAATGAAGCAGAGAAAGTGAACAGAGGCGGTGGAAGAAATTTGAGTGTGCTCC 4590
Db 4516 GACAAATGAAGCAGAGAAAGTGAACAGAGGCGGTGGAAGAAATTTGAGTGTGCTCC 4575
Qy 4591 GACGGGGATGTATTAATTCATGATGCGGTGCTTCCGAACTGCAAAATACGCCAA 4650
Db 4576 GACGGGGATGTATTAATTCATGATGCGGTGCTTCCGAACTGCAAAATACGCCAA 4635
Qy 4651 GCA----- 4653
Db 4636 GCAGATGTCCTAATCACTGAAGATGAATCAACCCGACACCACTGTGCCCCGG 4695
Qy 4654 ----- 4653
Db 4696 AGAACCTCTACTTGTGTAAGTCCAGCTTCCCTGACAAACAGCGTGGGTCAACCGCTTA 4755
Qy 4654 -----GAAAAACAGAACTGATGCTAACTG 4680
Db 4756 GAATCAGTTGTGCGAGGTGGAGAGTTTCTAGGGAAGAAAGCAGAGCTGATGCTAACTG 4815
Qy 4681 CTTGGAATCTCCCTGCTGAATACTGGAAGGTGATGACCGTCTGAGATGAATGCAAGCTG 4740
Db 4816 CTTGGAATCTCCCTGCTGAATACTGGAAGGTGATGACCGTCTGAGATGAATGCAAGCTG 4875
Qy 4741 CCCTTCACTGACAGAGGTGCTGTTGAGGCAACGAGAGAGGCTCTACCCCTGAAATGTC 4800
Db 4876 CCCTTCACTGACAGAGGTGCTGTTGAGGCAACGAGAGAGGCTCTACCCCTGAAATGTC 4935
Qy 4801 TTGAAAACCTCCCTTAACCATGATCCCAAGAAATGAGAGCTTTCGAAATTAATATATC 4860
Db 4936 TTGAAAACCTCCCTTAACCATGATCCCAAGAAATGAGAGCTTTCGAAATTAATATATC 4995
Qy 4861 AAGGACCTGAGAGAGTACTCATGATGAGAGAGAGAGGAGCTGTGTCTTGTGAGAC 4920
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Db 3121 ACCGAACGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3180
Qy 3151 TGGACATGCTGGAAGAACAGTCAATGATTTGAGAGCCCTAAACGATGAGCTGTAGAA 3210
Db 3181 TGGACATGCTGGAAGAACAGTCAATGATTTGAGAGCCCTAAACGATGAGCTGTAGAA 3240
Qy 3211 AAAGACGCGCAGTGGAGAGGCTTGAAGAGAGGCTCTGGGATGATGAAGTTCAGTTTGA 3270
Db 3241 AAAGACGCGCAGTGGAGAGGCTTGAAGAGAGGCTCTGGGATGATGAAGTTCAGTTTGA 3300
Qy 3271 TGTGGGATTCGAGAGCTGCAAGAAATGCTGACACCGAGAAACAGAGCAGGCGAGAGCC 3330
Db 3301 TGTGGGATTCGAGAGCTGCAAGAAATGCTGACACCGAGAAACAGAGCAGGCGAGAGCC 3360
Qy 3331 GATCAACGGAATCAACGAGTCTGCGCAGGTGATGAGTGAAGTGAAGTGAAGTGAAGTGA 3390
Db 3361 GATCAACGGAATCAACGAGTCTGCGCAGGTGATGAGTGAAGTGAAGTGAAGTGAAGTGA 3420
Qy 3391 GAGATTCTCGCTCTGAGAGAGGCTCTCAAGAGCAGAGCTGAAGGCGAGAGCTCTCT 3450
Db 3421 GAGATTCTCGCTCTGAGAGAGGCTCTCAAGAGCAGAGCTGAAGGCGAGAGCTCTCT 3480
Qy 3451 GACAGCTCAATGACCTGAGAGAGAGATGCTATGCTTGAATGAATGATGCTCCAGAGCTTA 3510
Db 3481 GACAGCTCAATGACCTGAGAGAGAGATGCTATGCTTGAATGAATGATGCTCCAGAGCTTA 3540
Qy 3511 CACCAAGAGCTGAGAGCTGAACGAGAGCTAAACAGAGGCTTCGGAAGAGCAAGCCAA 3570
Db 3541 CACCAAGAGCTGAGAGCTGAACGAGAGCTAAACAGAGGCTTCGGAAGAGCAAGCCAA 3600
Qy 3571 TTACAGCAGAGATGAGCTGACAGAAATCAATTTTCCGTGACTCAGAGATGCA 3630
Db 3601 TTACAGCAGAGATGAGCTGACAGAAATCAATTTTCCGTGACTCAGAGATGCA 3660

Qy 3631 GAAAGCTAGATCGGCTGATCTACTGAAGACAGAAAGATGACTTGGAGTATCAGCTG 3690
Db 3661 GAAAGCTAGATCGGCTGATCTACTGAAGACAGAAAGATGACTTGGAGTATCAGCTG 3720
Qy 3691 GAAACATTCAGATTCTCTATTCTCATGAAAGTGAAGAAATGAAAGGCACTATTTCTCA 3750
Db 3721 GAAACATTCAGATTCTCTATTCTCATGAAAGTGAAGAAATGAAAGGCACTATTTCTCA 3780
Qy 3751 CAAACCAATCTCATTTGATTTTCTGCAAGCCAAATGAGACCACTGCTTAAAAAGAAAG 3810
Db 3781 CAAACCAATCTCATTTGATTTTCTGCAAGCCAAATGAGACCACTGCTTAAAAAGAAAG 3838
Qy 3811 GGTATTATTAGTGAACGAAAGAGACCTGCTTTACCAACAAGGTTCTCTGACATGAC 3870
Db 3839 -----AGGTTCTCTGACATGAC 3855
Qy 3871 AATGAGCTGAGCTGAGCTGCTGAGAGAGAAAGCTGCTGTGACAGAGCTAGAGAGCC 3930
Db 3856 AATGAGCTGAGCTGAGCTGCTGAGAGAGAAAGCTGCTGTGACAGAGCTAGAGAGCC 3915
Qy 3931 CTTGAGAGACCCGATCGAGCTCCGGTCCGCCGAGAGAAAGCTGCCACCGCAAGCA 3990
Db 3916 CTTGAGAGACCCGATCGAGCTCCGGTCCGCCGAGAGAAAGCTGCCACCGCAAGCA 3975
Qy 3991 ACGGACCAACCCACACCAATCCAGCGGAGCCACCGGAGGACAGATGCGCATGTCGCGC 4050
Db 3976 ACGGACCAACCCACACCAATCCAGCGGAGCCACCGGAGGACAGATGCGCATGTCGCGC 4035
Qy 4051 ATCGTGCAGTCCGACAGAGACCAAGCCAGTGCATGAGCTGCTGCGCCCGCATCAGC 4110
Db 4036 ATCGTGCAGTCCGACAGAGACCAAGCCAGTGCATGAGCTGCTGCGCCCGCATCAGC 4095
Qy 4111 CCGAGAAAGAGTCTTCAATCTCCAGAGAAATTTAGTCCGCTTTAGGAGAGCATGAC 4170
Db 4096 CCGAGAAAGAGTCTTCAATCTCCAGAGAAATTTAGTCCGCTTTAGGAGAGCATGAC 4155
Qy 4171 CAACAATTCCTCAACCGATTCACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4230
Db 4156 CAACAATTCCTCAACCGATTCACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4215
Qy 4231 TGTCTGATACCGTGTGACCTTTGAGACGCGCAGGATCCAAATGTCGATGTCAAGTGA 4290
Db 4216 TGTCTGATACCGTGTGACCTTTGAGACGCGCAGGATCCAAATGTCGATGTCAAGTGA 4275
Qy 4291 TGTCAACCCCAAGTGTCAACGTCCTTCCAGCCACTGCGGCTTGTCTGCTGAATATGCC 4350
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Qy 4471 GGAAGCAAGGCTGGAGACAGAAATGATGTTGCTGAGAGGATCAAAAGTCTCATTTAT 4530
Db 4456 GGAAGCAAGGCTGGAGACAGAAATGATGTTGCTGAGAGGATCAAAAGTCTCATTTAT 4515
Qy 4531 GACAAAGAAAGCCAGAGAAATCTGAGACAGAGCGGATGAAGTGAAGTGAAGTGAAGTGA 4590
Db 4516 GACAAAGAAAGCCAGAGAAATCTGAGACAGAGCGGATGAAGTGAAGTGAAGTGAAGTGA 4575
Qy 4591 GACGGGATGATCTATTATGATGTCGTTTGGTCTTCCGAACTGCAATAACAGCCAA 4650
Db 4576 GACGGGATGATCTATTATGATGTCGTTTGGTCTTCCGAACTGCAATAACAGCCAA 4635
Qy 4651 GCA----- 4653
Db 4636 GCAGATGTCATATCATTAAGTGAAGTGAATCTCAACCGACACCACTGCTGGCCGGG 4695

QY	4654	-----	4655
Db	4656	AGAACCTTACTTGTCTAGCTCCAGCTTCCCTGACAAACAGCGTGGTCCACCGCTTAA	4755
QY	4654	-----	4655
Db	4756	GAATCAGTTGTGGCAGGTGGAGAGTTTCTAGGAGAAAAGCAGAAAGCTGATGCTAACTG	4815
QY	4681	CTTGGAAACTCCCTGCTGAAACTGGAAGGTGATGACCGTCTTAGACATGAATGACACGCTG	4740
Db	4816	CTTGGAAACTCCCTGCTGAAACTGGAAGGTGATGACCGTCTTAGACATGAATGACACGCTG	4875
QY	4741	CCCTTCAGTGAACCAAGTGTGTGTGGGGACCCGAGAAAGGCTTACGCTCGATGTTC	4800
Db	4876	CCCTTCAGTGAACCAAGTGTGTGTGGGGACCCGAGAAAGGCTTACGCTCGATGTTC	4935
QY	4801	TTGAAAAACTCCCTTAAACCACTGTCCCGAGAAATTGAGACAGTCTTCAATTAATTATTC	4866
Db	4936	TTGAAAAACTCCCTTAAACCACTGTCCCGAGAAATTGAGACAGTCTTCAATTAATTATTC	4995
QY	4861	AAGACCTGGAGAACTACTATGATAGCAGAGAAAGACGGGACCTGTGTCTTGTGAC	4920
Db	4996	AAGACCTGGAGAACTACTATGATAGCAGAGAAAGACGGGACCTGTGTCTTGTGAC	5055
QY	4921	GTGAAGAAAGTGAACAGTCCCTGGGCCAGTCCCACTGCTGCCACCGACATCTCA	4980
Db	5056	GTGAAGAAAGTGAACAGTCCCTGGGCCAGTCCCACTGCTGCCACCGACATCTCA	5115
QY	4981	CCCAACATTTTGTGAAGCTGTCAAGGGGCTGCCACTGTTGGGGGAGGAGAAATTGAGAC	5040
Db	5116	CCCAACATTTTGTGAAGCTGTCAAGGGGCTGCCACTGTTGGGGGAGGAGAAATTGAGAC	5175
QY	5041	GGGCTCTGCACTGTGAGCCATGCGCACCAAGTCCGCAAAAGTCCATCTTCCTCCGCTAACAGAAAC	5100
Db	5176	GGGCTCTGCACTGTGAGCCATGCGCACCAAGTCCGCAAAAGTCCATCTTCCTCCGCTAACAGAAAC	5235
QY	5101	CTCAGCAAAATCTGCATCCGGAAGAAGATAGAGACTTAGAGCCCTGACGCTGATCCAC	5160
Db	5236	CTCAGCAAAATCTGCATCCGGAAGAAGATAGAGACTTAGAGCCCTGACGCTGATCCAC	5295
QY	5161	TTCAACCAATTCAGATATCTCATTTGAGAACCAATTAATTCTACGAAATGACATGAACGAG	5220
Db	5296	TTCAACCAATTCAGATATCTCATTTGAGAACCAATTAATTCTACGAAATGACATGAACGAG	5355
QY	5221	TACAGCTCGAGAAATTCCTGATTAAGATGACATTCCTTGGGACCTGCTGTGTTGCC	5280
Db	5356	TACAGCTCGAGAAATTCCTGATTAAGATGACATTCCTTGGGACCTGCTGTGTTGCC	5415
QY	5281	GCCCTTTCGACAGCTTCCCTGTCTCAATCTGTGACGTTGAACAGCGACGACGAGAG	5340
Db	5416	GCCCTTTCGACAGCTTCCCTGTCTCAATCTGTGACGTTGAACAGCGACGACGAGAG	5475
QY	5341	GAGTACTTGCATGTGTTTCACGAATTTGGAATGTTCGGAATTCCTTACGGAAGACGTAGC	5400
Db	5476	GAGTACTTGCATGTGTTTCACGAATTTGGAATGTTCGGAATTCCTTACGGAAGACGTAGC	5535
QY	5401	CGCACAAGCATCTCAAGTGAAGTCGCTTACCTTGGGCTTTGGCTACAGAGAACCCTAT	5460
Db	5536	CGCACAAGCATCTCAAGTGAAGTCGCTTACCTTGGGCTTTGGCTACAGAGAACCCTAT	5595
QY	5461	CTGTGTTGTGACCCCACTTCAATCTACCTGGAAGTAATTGAGATCCAGGACCGCTCTGACGA	5520
Db	5596	CTGTGTTGTGACCCCACTTCAATCTACCTGGAAGTAATTGAGATCCAGGACCGCTCTGACGA	5655
QY	5521	GGGACCCCTGCGGAGGGGTACTGTGACATCCCGAACCCGCGCTACCTGGGCTCCGCAATT	5580
Db	5656	GGGACCCCTGCGGAGGGGTACTGTGACATCCCGAACCCGCGCTACCTGGGCTCCGCAATT	5715
QY	5581	TCCCTCAGAGAGCATTTTACTTGGGCTCTCCATACACAGATAAATTGAAGGCTATTGTGTCG	5640
Db	5716	TCCCTCAGAGAGCATTTTACTTGGGCTCTCCATACACAGATAAATTGAAGGCTATTGTGTCG	5775
QY	5641	AAGGAAAACCTCGTGAAGAGTCCGGGACCTGAACACCAACGGGGCCCGTCACTCCGCG	5700

[illegible]

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301 AGCTTTGAGTGTGTCACCTTGTGTAAGTCAGGTGTAAAGAGAAACCCGG 360
379 GACATCTATGCTATGAAAGTGAAGAAAGGCTTTATTTGGCCAGAGCAGTTTCA 438
361 GACATCTATGCTATGAAAGTGAAGAAAGGCTTTATTTGGCCAGAGCAGTTTCA 420
439 TTTTGTGAGAAAGAGCGAAACATATTTATCTGAAAGCAAGCCCGTGAATCCCCAATTA 498
421 TTTTGTGAGAAAGAGCGAAACATATTTATCTGAAAGCAAGCCCGTGAATCCCCAATTA 480
499 CAGTATGCTTTTCAAGACAAAATACCTTTATCTGAAAGCAAGCCCGTGAAGG 558
481 CAGTATGCTTTTCAAGACAAAATACCTTTATCTGAAAGCAAGCCCGTGAAGG 540
559 GACTTGCTGTCACTTTTGAATGATATGAGAGCAGTTAGTGAAGAACTGATACAGTTT 618
541 GACTTGCTGTCACTTTTGAATGATATGAGAGCAGTTAGTGAAGAACTGATACAGTTT 600
619 TACCTAGCTGAGCTGATTTTGTGCTTCAAGCGTTTCACTGATGGAATACGTGATGCA 678
601 TACCTAGCTGAGCTGATTTTGTGCTTCAAGCGTTTCACTGATGGAATACGTGATGCA 660
679 GACATCAAGCTGAGAAACATTTCTCGTTGACCGACAGACATCAACGTGTGTGATTTT 738
661 GACATCAAGCTGAGAAACATTTCTCGTTGACCGACAGACATCAACGTGTGTGATTTT 720
739 GGATCTGCGCGGAAATGAAATTCAAACAGATGTGTAATGCCAACTCCCGATTGGAGCC 798
721 GGATCTGCGCGGAAATGAAATTCAAACAGATGTGTAATGCCAACTCCCGATTGGAGCC 780
799 CCAAGATTACATGAGCTCTGAAAGTCTGACTGTGATGATGAACGGGATGAAAAGCATTAC 858
781 CCAAGATTACATGAGCTCTGAAAGTCTGACTGTGATGATGAACGGGATGAAAAGCATTAC 840
859 GGCCTGAGACTGTGATGCTGTGTGTCAGTGGGCGTGTATCTTATGAGATGATTTATGGGAGA 918
841 GGCCTGAGACTGTGATGCTGTGTGTCAGTGGGCGTGTATCTTATGAGATGATTTATGGGAGA 900
919 TCCCCCTTGCAGAGGGAACCTCTGCGCAAACTTCAATTAACATTATGAAATTTCCAGCGG 978
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1099 TCTAAATTTGATGAGAAACAACTTGTAACTCTCTCCCTTCTGTTCCACCTCAAG 1158
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1141 TCTGAGATGACCTTCAATTTTGAATGAACAGAGAAAGATTCGTGGTTCATCTCT 1200
1219 CCGTGCAGACTGAGCCCTCAGGCTTCTGGGTGAAGAACTGCGCTTTGTGGGTTTGG 1278
1201 CCGTGCAGACTGAGCCCTCAGGCTTCTGGGTGAAGAACTGCGCTTTGTGGGTTTGG 1260
1279 TACAGCAAGCACTGGGGAATTTCTGTAATGCTGAGTCTGTTGTGCGGATCTGACCTC 1338
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1459 GAGGTGAGAGCTGTGCTTATGTCAGAAAGAGGTGAGCTGAAGGCTTGAAGCTCAGAGA 1518
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1681 GTGGAAGAAATGAGGTGATGATGATCACTGTGGAAGAGATCTTGTCTCAGCAAGAA 1740
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1741 CGAGTGAATCTTCAAGAACTGAGGCTGAGAGAGTCTCGGCTTGTGTTGAATTTCAAG 1800
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1879 GTGGAAGAAATGAGGAACTGGAAGAAATCAATGCTGAGCAGACTCAAAATTTCAAG 1938
1861 GTGGAAGAAATGAGGAACTGGAAGAAATCAATGCTGAGCAGACTCAAAATTTCAAG 1920
1939 CTCGAAGAAATCTGAGAGAGCT----- 1962
1921 CTCGAAGAAATCTGAGAGAGCTTAAAGCCAGACAGAGGCCAGAGCTGCTGAG 1980
1963 -----GCAAGAGGAGCCGAGAGGAGCTGAGAGAGCTGAGAACTGAGAACTGAGAG 2010
1981 AATATCCGCAAGGCAAGAGAGGAGCCGAGAGGAGCTGAGAGAGCTGAGAACTGAGAG 2040
2011 GATTTCTTGAAGCAATCAAGAAAGAGTGTGGAAGCTGAGAAAGCTGAGAACTGAGAG 2070
2041 GATTTCTTGAAGCAATCAAGAAAGAGTGTGGAAGCTGAGAAAGCTGAGAACTGAGAG 2100
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2131 ATTCAGACAAATTCCAACAGATTCAGAGAGATGCTGATTAATTTCTGAGCTGAGAG 2190
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2161 ATTCAGACAAATTCCAACAGATTCAGAGAGATGCTGATTAATTTCTGAGCTGAGAG 2220
2191 AAACATCGGAGGCGCAAGTCTCAGCCAGCAGCTGAAGATGCACTTGAAGCAAGAG 2250
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Qy 2731 CTACAGCTCTCCCTGACAGAGCGGAGTCAAGTTGACAGCCCTGACAGGCTGACAGGCG 2790
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4651 GCA----- 4653
4636 GCAGATGTCCCATACATCTAGGAAGTGAATCTCACCCGACACACCTGCTGCCCCGG 4695
4654 ----- 4653
4696 AGAACCTTACTTGTAGCTCCAGCTTCCCTGACAAAGAGGCTGGTCAACGCCCTTA 4755
4654 ----- GAAAAGCAGAGCTGATGCTAACTG 4680
4756 GAATCATGTTCTCCAGGTGGAGAGTTTCTAGGGAAAAAAGCAGAGCTGATGCTAACTG 4815
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4741 CCTTCAGTACAGGAGT 4800
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4801 TTGAAAACTCCCTAACCCATGCTCCAGAAATTGAGACAGTCTTCCAAATTTATTTATC 4860
4936 TTGAAAACTCCCTAACCCATGCTCCAGAAATTGAGACAGTCTTCCAAATTTATTTATC 4995
4861 AAGACCTGGAGAGCTACTCATATGATGAGAGAAAGGGGCACTGTGTCTTTGTGAC 4820
4996 AAGACCTGGAGAGCTACTCATATGATGAGAGAAAGGGGCACTGTGTCTTTGTGAC 5055
4921 GTGAAAGAGTGAAGAGTCCCTGAGCCAGTCCCACTGCTCCAGCCGACATCTCA 4980
5056 GTGAAAGAGTGAAGAGTCCCTGAGCCAGTCCCACTGCTCCAGCCGACATCTCA 5115
4981 CCCAATTTTGAAGCTGTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5040
5116 CCCAATTTTGAAGCTGTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5175
5041 GGGCTGTGATCTGTGACAGGCAAGCCAGCAAGAGTGTCTTTCCGCTTCAACGAAAC 5100
5176 GGGCTGTGATCTGTGACAGGCAAGCCAGCAAGAGTGTCTTTCCGCTTCAACGAAAC 5235
5101 CTGAGCAATTAATCTGATCTCGGAAAGAGATGAGACCTCAGAGCCCTGAGCTTATCCAC 5160
5236 CTGAGCAATTAATCTGATCTCGGAAAGAGATGAGACCTCAGAGCCCTGAGCTTATCCAC 5295
5161 TTCAACAATTAATCTGATCTCGGAAAGAGATGAGACCTTCAAGAAATCGACATGAAGCAG 5220
5296 TTCAACAATTAATCTGATCTCGGAAAGAGATGAGACCTTCAAGAAATCGACATGAAGCAG 5355
5221 TACAGCCTGAGAGATTTCTGATTAAGATGAGACCTTCTGGACCTGCTGTGTGTGCC 5280
5356 TACAGCCTGAGAGATTTCTGATTAAGATGAGACCTTCTGGACCTGCTGTGTGTGCC 5415
5281 GCGCTTTCGCAAGCTTCCCTGCTCAATGATGAGTGAAGAGAGGAGGAGGAGGAGGAG 5340
5416 GCGCTTTCGCAAGCTTCCCTGCTCAATGATGAGTGAAGAGAGGAGGAGGAGGAGGAG 5475
5341 GAGTACTTGT 5400
5476 GAGTACTTGT 5535
5401 CGACAGAGAGATTTCAAGTGAAGTGGCTTACCTTTGGCCCTTTCACAGAGAACCTCTAT 5460
5536 CGACAGAGAGATTTCAAGTGAAGTGGCTTACCTTTGGCCCTTTCACAGAGAACCTCTAT 5595
5461 CTGTGTGTGACCACTTCAACTCACTCGAAGTAAATTGAGATCCAGGAGAGCTCTGAGCA 5520
5596 CTGTGTGTGACCACTTCAACTCACTCGAAGTAAATTGAGATCCAGGAGAGCTCTGAGCA 5655
5521 GGGAGCCCTGAGCCGAGAGCTGAGCATCTCGAAGCCGAGCTAAGCTGAGCCCTGAGCAT 5580
5656 GGGAGCCCTGAGCCGAGAGCTGAGCATCTCGAAGCCGAGCTAAGCTGAGCCCTGAGCAT 5715

QY 5581 TCCTCAGAGAGCATTTACTTGGGCTCTCATACAGATAAATTAAGGATCTTCTGCG 5640
DB 5716 TCCTCAGAGAGCATTTACTTGGGCTCTCATACAGATAAATTAAGGATCTTCTGCG 5775
QY 5641 AAGGAAACCTGCTGAAGAGTCCGCACTGAACACACCGGAGCCGCTCACTTCCCG 5700
DB 5776 AAGGAAACCTGCTGAAGAGTCCGCACTGAACACACCGGAGCCGCTCACTTCCCG 5835
QY 5701 AG 5702
DB 5836 AG 5837

RESULT 3

US-09-804-471A-1
; Sequence 1, Application US/09804471A
; Patent No. 6479269
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCES: CL001164
; CURRENT APPLICATION NUMBER: US/09/804,471A
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 1
; TYPE: DNA
; LENGTH: 1515
; ORGANISM: Human
US-09-804-471A-1

Query Match 21.3%; Score 1397.8; DB 4; Length 1515;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1402; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 13 GGGAGATTTGAAGTTCAAATATGAGAGCGGGAATCCTTTGATGCTGTGCTGAA 72
DB 1 GGGAGATTTGAAGTTCAAATATGAGAGCGGGAATCCTTTGATGCTGTGCTGAA 60
QY 73 CCATTTGCGAGCGGCGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACACCTTTATG 132
DB 61 CCATTTGCGAGCGGCGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACACCTTTATG 120
QY 133 ACTCAACAGCAGATGTCTCTCTTTCCGAGAGGAGATTAAGATGCTCTTTGTTCTC 192
DB 121 ACTCAACAGCAGATGTCTCTCTTTCCGAGAGGAGATTAAGATGCTCTTTGTTCTC 180
QY 193 TTTGAAGATGAGTCAAGCTGCTCTGATGAAGATTAAGACGTGACAACTTTGTCCG 252
DB 181 TTTGAAGATGAGTCAAGCTGCTCTGATGAAGATTAAGACGTGACAACTTTGTCCG 240
QY 253 AAGTATTCGAGACCATATGCTAGTTACAGAGCTCCAGCCTTCCGCAAGGACTTCGAA 312
DB 241 AAGTATTCGAGACCATATGCTAGTTACAGAGCTCCAGCCTTCCGCAAGGACTTCGAA 300
QY 313 GTCAGAGCTTGTAGT 372
DB 301 GTCAGAGCTTGTAGT 360
QY 373 ACCGGGACATTTATGCTATGAAGTGAAGAGAGCTTTATTTGGCCAGAGAGCAG 432
DB 361 ACCGGGACATTTATGCTATGAAGTGAAGAGAGCTTTATTTGGCCAGAGAGCAG 420
QY 433 GTTTCATTTTGAAGAGAGGAGGAAATATTTATCTGAAAGCAAGCCGCTGATCCCG 492
DB 421 GTTTCATTTTGAAGAGAGGAGGAAATATTTATCTGAAAGCAAGCCGCTGATCCCG 480
QY 493 CAATTAAGATGCTCTTTCAGAGCAAAATATCACTTTATCTGATGAGAGAAATATGAGCT 552
DB 481 CAATTAAGATGCTCTTTCAGAGCAAAATATCACTTTATCTGATGAGAAATATGAGCT 540

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QY 553 GGAAGGGAATTGCTGCTCACTTTGATATAGAGACCACTAGATGAAAACCTGATA 612
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Db 541 GGAAGGGAATTGCTGCTCACTTTGATATAGAGACCACTAGATGAAAACCTGATA 600
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QY 613 CAGTTTACCTGCTGAGCTGATTTGGCTGTTCAAGGCTTCATGTAGGATACGTG 672
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Db 601 CAGTTTACCTGCTGAGCTGATTTGGCTGTTCAAGGCTTCATGTAGGATACGTG 660
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QY 673 CATCGAGACATCAAGCTTGAGAACATTCCTGTTACCGACAGAGACATCAAGCTGTG 732
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Db 661 CATCGAGACATCAAGCTTGAGAACATTCCTGTTACCGACAGAGACATCAAGCTGTG 720
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QY 733 GATTTTGGATCTGCCCCGGAATAATGATTCAAACAAATGTGAATCCCAAATCCCGGAT 792
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Db 721 GATTTTGGATCTGCCCCGGAATAATGATTCAAACAAATGTGAATCCCAAATCCCGGAT 780
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QY 793 GGGACCCCAAGATTACATAGGCTCTGAAAGCTGACCTGTATGAAACGGGATGGAAGAGC 852
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Db 781 GGGACCCCAAGATTACATAGGCTCTGAAAGCTGACCTGTATGAAACGGGATGGAAGAGC 840
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QY 853 ACCTACGGCTGAGCTGTGACCTGTGATGAGTGGGCTGATGCTATGATGATTTAT 912
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Db 841 ACCTACGGCTGAGCTGTGACCTGTGATGAGTGGGCTGATGCTATGATGATTTAT 900
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QY 913 GGGAGATCCCCCTTCCGAGAGGGAACCTCTGCGAAGACCTTCAATTAATTAATTTTC 972
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Db 901 GGGAGATCCCCCTTCCGAGAGGGAACCTCTGCGAAGACCTTCAATTAATTAATTTTC 960
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QY 973 CAGCGGTTTTGAAATTTCCAGATGACCCCAAGTGAAGTACTTTCTTGATCTGATT 1032
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Db 961 CAGCGGTTTTGAAATTTCCAGATGACCCCAAGTGAAGTACTTTCTTGATCTGATT 1020
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QY 1033 CAAAGCTTGTGTGCGGCCAGAAAGAGACCTGAAGTTTGAAGTCTTGTCTCCATCT 1092
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Db 1021 CAAAGCTTGTGTGCGGCCAGAAAGAGACCTGAAGTTTGAAGTCTTGTCTCCATCT 1080
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QY 1093 TTCTCTCTTAAATTTGATCTGGAACAACATTCGTACTCTCTCCCTTCTGTTCCACC 1152
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Db 1081 TTCTCTCTTAAATTTGATCTGGAACAACATTCGTACTCTCTCCCTTCTGTTCCACC 1140
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QY 1153 CTCAAGCTGACGATGACACCTCCAAATTTGATGAACAGAGAAGAAATTCGTGGATTCA 1212
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Db 1141 CTCAAGCTGACGATGACACCTCCAAATTTGATGAACAGAGAAGAAATTCGTGGATTCA 1200
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QY 1213 TCCTCTCCGTGCGACGCTGAGCCCTCAGGCTTCTCCGGTGAAGAATCTGCCGTTTGTGGG 1272
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Db 1201 TCCTCTCCGTGCGACGCTGAGCCCTCAGGCTTCTCCGGTGAAGAATCTGCCGTTTGTGGG 1260
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QY 1273 TTTTTCGTAAGCAAGGCACTGGGGATCTTGATGATCTGATCTGTTGTGCGGGCTG 1332
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Db 1261 TTTTTCGTAAGCAAGGCACTGGGGATCTTGATGATCTGATCTGTTGTGCGGGCTG 1320
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QY 1333 GACTCCCCCTGCAAGACTAGCTCCATGAGAAAGAACTTCTCATCAAAAGCAAGAGCTA 1392
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Db 1321 GACTCCCCCTGCAAGACTAGCTCCATGAGAAAGAACTTCTCATCAAAAGCAAGAGCTA 1380
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QY 1393 CAAGACTCTGAGCAAGTGTCAACAAT 1421
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Db 1381 CAAGACTCTGAGCAAGTGTCAACAAGT 1409
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RESULT 4
US-10-238-709-1
; Sequence 1, Application US/10238709
; Patent No. 6680188
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164D1V
; CURRENT APPLICATION NUMBER: US/10/238,709
; CURRENT FILING DATE: 2002-09-11
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NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Human
US-10-238-709-1

Query Match      21.3%; Score 1397.8; DB 4; Length 1515;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1402; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 13 GGGAGATGTTGAAGTTCAATATAGAGCGCGGAATCTTTGATGCTGTGCTGTA 72
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Db 1 GGGAGATGTTGAAGTTCAATATAGAGCGCGGAATCTTTGATGCTGTGCTGTA 60
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QY 73 CCCATTGCGAAGCCGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAACCAACCTTTATG 132
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Db 61 CCCATTGCGAAGCCGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAACCAACCTTTATG 120
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    |||
QY 133 ACTCAACGACGATGCTCCCTCTTCCGGAAGGGAATTAAGTCCCTCTTGTGCTC 192
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Db 121 ACTCAACGACGATGCTCCCTCTTCCGGAAGGGAATTAAGTCCCTCTTGTGCTC 180
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QY 193 TTTGAAGATGACAGCTCAGCTGCTCTGATGAAGATTAAGACGTGAGCACTTTGTCCG 252
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Db 181 TTTGAAGATGACAGCTCAGCTGCTCTGATGAAGATTAAGACGTGAGCACTTTGTCCG 240
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QY 253 AAGTATTCGACACCATAGCTGATTAAGAGAGCTCCAGCTTGGCAAAGACTTCGA 312
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Db 241 AAGTATTCGACACCATAGCTGATTAAGAGAGCTCCAGCTTGGCAAAGACTTCGA 300
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QY 313 GTCAAGATCTTGATGTTGTGCTCACTTGTGTAAGTGAAGTGTAAAGAGAAAGCA 372
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Db 301 GTCAAGATCTTGATGTTGTGCTCACTTGTGTAAGTGAAGTGTAAAGAGAAAGCA 360
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QY 373 ACCGGGACATCTATGCTATGAAGATGAAGAAAGGCTTTATTTGGCCAGAGCAG 432
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Db 361 ACCGGGACATCTATGCTATGAAGATGAAGAAAGGCTTTATTTGGCCAGAGCAG 420
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QY 433 GTTTCATTTTTGAGGAAGAGCGGAACATATTTCTGAGACCAAGCCCTGTATCCC 492
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Db 421 GTTTCATTTTTGAGGAAGAGCGGAACATATTTCTGAGACCAAGCCCTGTATCCC 480
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QY 493 CAATTACGATAGCCTTTCAAGCAAAATACCTTTATCTGATGAGAAATATCAGCT 552
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Db 481 CAATTACGATAGCCTTTCAAGCAAAATACCTTTATCTGATGAGAAATATCAGCT 540
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QY 553 GGAAGGGAATTGCTGTCACTTTGATGATGAAGACCACTTATGATGAAGAAACCTGATA 612
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Db 541 GGAAGGGAATTGCTGTCACTTTGATGATGAAGACCACTTATGATGAAGAAACCTGATA 600
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QY 613 CAGTTTACCTTACGCTGAGCTGATTTTGGCTGTTCACAGCTTCATCTGATGGATACGTG 672
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Db 601 CAGTTTACCTTACGCTGAGCTGATTTTGGCTGTTCACAGCTTCATCTGATGGATACGTG 660
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QY 673 CATCGAGACATCAAGCTTGAGAACATTCCTGTTACCGACAGAGACATCAAGCTGTG 732
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    |||
Db 661 CATCGAGACATCAAGCTTGAGAACATTCCTGTTACCGACAGAGACATCAAGCTGTG 720
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QY 733 GATTTTGGATCTGCCCCGGAATAATGATTCAAACAAATGTGAATCCCAAATCCCGGAT 792
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Db 721 GATTTTGGATCTGCCCCGGAATAATGATTCAAACAAATGTGAATCCCAAATCCCGGAT 780
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QY 793 GGGACCCCAAGATTACATAGGCTCTGAAAGCTGACCTGTGATGAACGGGATGGAAGAGC 852
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    |||
Db 781 GGGACCCCAAGATTACATAGGCTCTGAAAGCTGACCTGTGATGAACGGGATGGAAGAGC 840
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QY 853 ACCTACGGCTGAGCTGTGATGCTGTGATGAGTGGGCTGATGCTATGATGATTTAT 912
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Db 841 ACCTACGGCTGAGCTGTGATGCTGTGATGAGTGGGCTGATGCTATGATGATTTAT 900
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QY 913 GGGAGATCCCCCTTCCGAGAGGGAACCTCTGCGAAGAACCTTCAATTAATTAATTTTC 972
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Db 901 GGGAGATCCCTTCCAGAGGGAACCTGCGCAAGAACCTTCAATTAATGATTTTC 960
Qy 973 CAGCGGTTTTGAATTTCCAGATGACCCCAAGATGACAGTCTTTGATCTGATT 1032
Db 961 CAGCGGTTTTGAATTTCCAGATGACCCCAAGATGACAGTCTTTGATCTGATT 1020
Qy 1033 CAAAGCTTGTTGGGCGCAAGAGAGAGTGAAGTTGATCTTTGCTGGCATTCCT 1092
Db 1021 CAAAGCTTGTTGGGCGCAAGAGAGAGTGAAGTTGATCTTTGCTGGCATTCCT 1080
Qy 1093 TTCTTCTAAATTTAGCTGGAACAACATTCGTAATCTCTCCCTTCGTTCCACC 1152
Db 1081 TTCTTCTAAATTTAGCTGGAACAACATTCGTAATCTCTCCCTTCGTTCCACC 1140
Qy 1153 CTCAGTCTGACGATGACATCTTCAAATTTGATGAACAGAGAAATTCGCGTTTCA 1212
Db 1141 CTCAGTCTGACGATGACATCTTCAAATTTGATGAACAGAGAAATTCGCGTTTCA 1200
Qy 1213 TCCTCTCGGTGCGAGCTGAGCCCTCAGGCTTCTCGGCTGAAGAACTGCGCTTGTGGG 1272
Db 1201 TCCTCTCGGTGCGAGCTGAGCCCTCAGGCTTCTCGGCTGAAGAACTGCGCTTGTGGG 1260
Qy 1273 TTTTCCTAGAGCAAGGCACTGCGGATTTCTGTAGATCTGATCTGTGTGCGGCTTG 1332
Db 1261 TTTTCCTAGAGCAAGGCACTGCGGATTTCTGTAGATCTGATCTGTGTGCGGCTTG 1320
Qy 1333 GACTCCCTGCGCAAGCACTGCTCATGAGAAAGAACTTCTCATCAAAAGCAAGCTA 1392
Db 1321 GACTCCCTGCGCAAGCACTGCTCATGAGAAAGAACTTCTCATCAAAAGCAAGCTA 1380
Qy 1393 CAAGACTCTCAGAGCAAGTGTCAAGAT 1421
Db 1381 CAAGACTCTCAGAGCAAGTGTCAAGAT 1409
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RESULT 5

US-09-774-528-419

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/ Sequence 419, Application US/09774528
/ Patent No. 6743619
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Zhou, Ping
/ APPLICANT: Goodrich, Ryle
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Ren, Feiyun
/ APPLICANT: Asundi, Vinod
/ APPLICANT: Zhang, Jie
/ APPLICANT: Zhao, Qing A.
/ APPLICANT: Yang, Yonghong
/ APPLICANT: Xue, Aidong J.
/ APPLICANT: Wehrman, Tom
/ APPLICANT: Wang, Jian-Rui
/ APPLICANT: Wang, Dunrui
/ APPLICANT: Drmanac, Radoje T.
/ TITLE OF INVENTION: No. 6743619el Nucleic Acids and
/ FILE REFERENCE: Polypeptides
/ CURRENT APPLICATION NUMBER: US/09/774,528
/ CURRENT FILING DATE: 2001-01-30
/ NUMBER OF SEQ ID NOS: 441
/ SOFTWARE: pf_genes Version 2.0
/ SEQ ID NO 419
/ LENGTH: 2162
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (364)..(2010)
US-09-774-528-419
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Query Match 14.7%; Score 965.6; DB 4; Length 2162;
Best Local Similarity 99.1%; Pred. No. 1.8e-264;

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Matches 971; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 1 AGAGCCGCGCAGTGGGAGATGTTGAAGTTCAATATAGAGCCCGGAATCCCTTTGATGCT 60
Db 346 AATGCGCCAGTGGGAGATGTTGAAGTTCAATATAGAGCCCGGAATCCCTTTGATGCT 405
Qy 61 GGTGCTGTAACCCATTGSCCAGCCGCGCTCCAGGCTGAATCTGTTCTCCAGGGGAAA 120
Db 406 GGTGCTGTAACCCATTGSCCAGCCGCGCTCCAGGCTGAATCTGTTCTCCAGGGGAAA 465
Qy 121 CCACCTTTATAGTCAACAGAGATGTCCTCTCTTCCGAAAGGATTAATAGTGC 180
Db 466 CCACCTTTATAGTCAACAGAGATGTCCTCTCTTCCGAAAGGATTAATAGTGC 525
Qy 181 CTCTTGTCTCTTTGAAGAAATGCAATGCTGCTCTGATGAATTAAGACGTGAC 240
Db 526 CTCTTGTCTCTTTGAAGAAATGCAATGCTGCTCTGATGAATTAAGACGTGAC 585
Qy 241 AACTTGTCCGAGAGATTCGAGACATAGCTGAGTTACAGAGCTCCAGCTTCGGA 300
Db 586 AACTTGTCCGAGAGATTCGAGACATAGCTGAGTTACAGAGCTCCAGCTTCGGA 645
Qy 301 AAGACTTGAAGTCAAGAGTCTTGAAGTTGCTCACTTGTGAAGTGAAGTGA 360
Db 646 AAGACTTGAAGTCAAGAGTCTTGAAGTTGCTCACTTGTGAAGTGAAGTGA 705
Qy 361 AAGAGAAAGCAACCGGAGCATCTATGCTATGAAGATGAAGAAAGGCTTTATTG 420
Db 706 AAGAGAAAGCAACCGGAGCATCTATGCTATGAAGATGAAGAAAGGCTTTATTG 765
Qy 421 GCCAGAGCAGATTTCAATTTTGAAGAAAGCGGAAACATTTATCTGAAGACAAAC 480
Db 766 GCCAGAGCAGATTTCAATTTTGAAGAAAGCGGAAACATTTATCTGAAGACAAAC 825
Qy 481 CCGTGAATCCCAATTAACAGTATGCTTTCAGACAATAATCACCTTATCTGAG 540
Db 826 CCGTGAATCCCAATTAACAGTATGCTTTCAGACAATAATCACCTTATCTGAG 885
Qy 541 GAATATCAGCTGAGGGGACTTGTCTGATCTTTGAATGATATGAGGACCAATTAGT 600
Db 886 GAATATCAGCTGAGGGGACTTGTCTGATCTTTGAATGATATGAGGACCAATTAGT 945
Qy 601 GAAACCTGATCAGTTTAACTAGCTGAGCTGATTTGGCTGTTCAAGGCTTATCTG 660
Db 946 GAAACCTGATCAGTTTAACTAGCTGAGCTGATTTGGCTGTTCAAGGCTTATCTG 1005
Qy 661 ATGGATACGTCATCGAGACATCAAGCTGGAACATTCCTGTTGACCGCACAGACAC 720
Db 1006 ATGGATACGTCATCGAGACATCAAGCTGGAACATTCCTGTTGACCGCACAGACAC 1065
Qy 721 ATCAAGCTGTGATTTTGAATCTGCTGCGGAAATGAATTAACAGATGTGAATGCC 780
Db 1066 ATCAAGCTGTGATTTTGAATCTGCTGCGGAAATGAATTAACAGATGTGAATGCC 1125
Qy 781 AAACCTCCGATTTGGAGCCCAATTAACATAGCTCTCGAAGTCTGATGTGAACGGG 840
Db 1126 AAACCTCCGATTTGGAGCCCAATTAACATAGCTCTCGAAGTCTGATGTGAACGGG 1185
Qy 841 GATGAAAAAGCACTGAGCTGAGCTGATGCTGTGCTGAGTGGCGCTGATTCCTAT 900
Db 1186 GATGAAAAAGCACTGAGCTGAGCTGATGCTGTGCTGAGTGGCGCTGATTCCTAT 1245
Qy 901 GAGATGATTTATGGAAGATCCCTTTCGAGAGGGAACCTCTGCGAATCTTCAATAC 960
Db 1246 GAGATGATTTATGGAAGATCCCTTTCGAGAGGGAACCTCTGCGAATCTTCAATAC 1305
Qy 961 ATTATGAATTTCCAGGTT 980
Db 1306 ATTATGAATTTCCAGGTT 1325
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RESULT 6

US-09-916-204-1

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/ Sequence 1, Application US/09916204
/ Patent No. 6638745
/ GENERAL INFORMATION:
/ APPLICANT: WEI, Ming-Hui et al.
/ TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
/ TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
/ TITLE OF INVENTION: THEREOF
/ FILE REFERENCE: CL001164CIP
/ CURRENT APPLICATION NUMBER: US/09/916,204
/ CURRENT FILING DATE: 2001-07-24
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 1133
/ TYPE: DNA
/ ORGANISM: Human
US-09-916-204-1

Query Match      11.7%; Score 768; DB 4; Length 1133;
Best Local Similarity 99.4%; Pred. No. 3.1e-208;
Matches 771; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 AGAGCCGCCAGTGGGAGATGTGAAGTCAATATGAGCGCGAATCCTTGATGCT 60
DB      36 AGAGCCGCCAGTGGGAGATGTGAAGTCAATATGAGCGCGAATCCTTGATGCT 95
QY      61 GGTGCTGTGAACCCATTGCGACCGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAA 120
DB      96 GGTGCTGTGAACCCATTGCGACCGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAA 155
QY      121 CGACCCCTTATGACTCAACAGAGATGTCTCTCTTCCGAGAAAGGATTTAGATGCC 180
DB      156 CCACCCCTTATGACTCAACAGAGATGTCTCTCTTCCGAGAAAGGATTTAGATGCC 215
QY      181 CTCTTGTCTCTTTGAGAGATCAAGTCAAGCTGCTCTGATGAAGATTAAGCAGTGA 240
DB      216 CTCTTGTCTCTTTGAGAGATCAAGTCAAGCTGCTCTGATGAAGATTAAGCAGTGA 275
QY      241 AACTTTGTCGGAAGTATTCGACACCAATAGCTGATTAAGAGACTCCAGCTTGGCA 300
DB      276 AACTTTGTCGGAAGTATTCGACACCAATAGCTGATTAAGAGACTCCAGCTTGGCA 335
QY      301 AAGGACTTCGAAAGTCAAGAGTCTTGTAGTGTGTGATCACTTGTGAAGTGAAGG 360
DB      336 AAGGACTTCGAAAGTCAAGAGTCTTGTAGTGTGTGATCACTTGTGAAGTGAAGG 395
QY      361 AAGAGAGAAAGCAACCGGGGACATCTATGCTATGAAGATGAAGAAAGGCTTTATTG 420
DB      396 AAGAGAGAAAGCAACCGGGGACATCTATGCTATGAAGATGAAGAAAGGCTTTATTG 455
QY      421 GCCCAGAGACAGGTTTCAATTTTGAAGAGAGCGGAACTATTTATCTGAAGCAAGC 480
DB      456 GCCCAGAGACAGGTTTCAATTTTGAAGAGAGCGGAACTATTTATCTGAAGCAAGC 515
QY      481 CCGTGATCCGCCAATTAAGTATGACCTTCAGGACAAAATCACTTTATCTGATGAG 540
DB      516 CCGTGATCCGCCAATTAAGTATGACCTTCAGGACAAAATCACTTTATCTGATGAG 575
QY      541 GAATATCAGCTCGAGGGGACTTGCTGTCACTTTTGAATAGATAGAGCAAGTTAGAT 600
DB      576 GAATATCAGCTCGAGGGGACTTGCTGTCACTTTTGAATAGATAGAGCAAGTTAGAT 635
QY      601 GAAAACTGATACAGTTTATCTAGCTGAGTGAATTTGGCTGTTCACAGCTTCATCTG 660
DB      636 GAAAACTGATACAGTTTATCTAGCTGAGTGAATTTGGCTGTTCACAGCTTCATCTG 695
QY      661 ATGGGATACGTCATCGACATCAAGCTGAGAACTTCGTTGACCGACAGAGAC 720
DB      696 ATGGGATACGTCATCGACATCAAGCTGAGAACTTCGTTGACCGACAGAGAC 755
QY      721 ATCAAGCTGTGATTTTGTGATCTGCGCGAAAATGAATCAACAGATGTGAA 776
DB      756 ATCAAGCTGTGATTTTGTGATCTGCGCGAAAATGAATCAACAGATGTGAA 811
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RESULT 7
US-10-282-048-1
/ Sequence 1, Application US/10282048
/ Patent No. 6692948
/ GENERAL INFORMATION:
/ APPLICANT: WEI, Ming-Hui et al.
/ TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
/ TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
/ TITLE OF INVENTION: THEREOF
/ FILE REFERENCE: CL001164CIP-DIV
/ CURRENT APPLICATION NUMBER: US/10/282,048
/ CURRENT FILING DATE: 2002-10-29
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 1133
/ TYPE: DNA
/ ORGANISM: Human
US-10-282-048-1

Query Match      11.7%; Score 768; DB 4; Length 1133;
Best Local Similarity 99.4%; Pred. No. 3.1e-208;
Matches 771; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 AGAGCCGCCAGTGGGAGATGTGAAGTCAATATGAGCGCGAATCCTTGATGCT 60
DB      36 AGAGCCGCCAGTGGGAGATGTGAAGTCAATATGAGCGCGAATCCTTGATGCT 95
QY      61 GGTGCTGTGAACCCATTGCGACCGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAA 120
DB      96 GGTGCTGTGAACCCATTGCGACCGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAA 155
QY      121 CGACCCCTTATGACTCAACAGAGATGTCTCTCTTCCGAGAAAGGATTTAGATGCC 180
DB      156 CCACCCCTTATGACTCAACAGAGATGTCTCTCTTCCGAGAAAGGATTTAGATGCC 215
QY      181 CTCTTGTCTCTTTGAGAGATCAAGTCAAGCTGCTCTGATGAAGATTAAGCAGTGA 240
DB      216 CTCTTGTCTCTTTGAGAGATCAAGTCAAGCTGCTCTGATGAAGATTAAGCAGTGA 275
QY      241 AACTTTGTCGGAAGTATTCGACACCAATAGCTGATTAAGAGACTCCAGCTTGGCA 300
DB      276 AACTTTGTCGGAAGTATTCGACACCAATAGCTGATTAAGAGACTCCAGCTTGGCA 335
QY      301 AAGGACTTCGAAAGTCAAGAGTCTTGTAGTGTGTGATCACTTGTGAAGTGAAGG 360
DB      336 AAGGACTTCGAAAGTCAAGAGTCTTGTAGTGTGTGATCACTTGTGAAGTGAAGG 395
QY      361 AAGAGAGAAAGCAACCGGGGACATCTATGCTATGAAGATGAAGAAAGGCTTTATTG 420
DB      396 AAGAGAGAAAGCAACCGGGGACATCTATGCTATGAAGATGAAGAAAGGCTTTATTG 455
QY      421 GCCCAGAGACAGGTTTCAATTTTGAAGAGAGCGGAACTATTTATCTGAAGCAAGC 480
DB      456 GCCCAGAGACAGGTTTCAATTTTGAAGAGAGCGGAACTATTTATCTGAAGCAAGC 515
QY      481 CCGTGATCCGCCAATTAAGTATGACCTTCAGGACAAAATCACTTTATCTGATGAG 540
DB      516 CCGTGATCCGCCAATTAAGTATGACCTTCAGGACAAAATCACTTTATCTGATGAG 575
QY      541 GAATATCAGCTCGAGGGGACTTGCTGTCACTTTTGAATAGATAGAGCAAGTTAGAT 600
DB      576 GAATATCAGCTCGAGGGGACTTGCTGTCACTTTTGAATAGATAGAGCAAGTTAGAT 635
QY      601 GAAAACTGATACAGTTTATCTAGCTGAGTGAATTTGGCTGTTCACAGCTTCATCTG 660
DB      636 GAAAACTGATACAGTTTATCTAGCTGAGTGAATTTGGCTGTTCACAGCTTCATCTG 695
QY      661 ATGGGATACGTCATCGACATCAAGCTGAGAACTTCGTTGACCGACAGAGAC 720
DB      696 ATGGGATACGTCATCGACATCAAGCTGAGAACTTCGTTGACCGACAGAGAC 755
```

QY 721 ATCAAGTGTGATTTTGGATCTGCGGAGAAATGAATTCAAACAGATGTGAA 776
Db 756 ATCAAGTGTGATTTTGGATCTGCGGAGAAATGAATTCAAACAGATGTGAA 811

RESULT 8

US-09-949-016-2533/C
Sequence 2533, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ. ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ. ID NO 2533
LENGTH: 2188
TYPE: DNA
ORGANISM: Human
US-09-949-016-2533

Query Match 8.7%; Score 570; DB 4; Length 2188;
Best Local Similarity 100.0%; Pred. No. 1.9e-151;

Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6005 AGGAGAGAGGCGAGAGTGCCTCTCAAGTTTCACGGTTAACTGTCACCTATTATGACT 6064
Db 1771 AGGAGAGAGGCGAGAGTGCCTCTCAAGTTTCACGGTTAACTGTCACCTATTATGACT 1712
QY 6065 GGAATATAAAGCTGGAACAACCTGCACTGCTGAGATCATCCAGCTGA 6124
Db 1711 GGAATATAAAGCTGGAACAACCTGCACTGCTGAGATCATCCAGCTGA 1652
QY 6125 ATGGAATAATCCGGGACGAGTTGAAAAGTCTGTCGAGAACAGATTATTCGTCGACG 6184
Db 1651 ATGGAATAATCCGGGACGAGTTGAAAAGTCTGTCGAGAACAGATTATTCGTCGACG 1592
QY 6185 AGTTCAATGTAAGTCTGAGACGTGTAATTAATAAATGAGCTTAAGGCTGACAGCCAGC 6244
Db 1591 AGTTCAATGTAAGTCTGAGACGTGTAATTAATAAATGAGCTTAAGGCTGACAGCCAGC 1532
QY 6245 CACCTCTGCTTACAAAAGAGTACTTAGTCACATGACTGTAAAGAAACAATTGTAAACC 6304
Db 1531 CACCTCTGCTTACAAAAGAGTACTTAGTCACATGACTGTAAAGAAACAATTGTAAACC 1472
QY 6305 TCATCTAGAAATCAGAAAGCTTCTAATTTATAGAAATGACCTTCCTGAGCCGAGA 6364
Db 1471 TCATCTAGAAATCAGAAAGCTTCTAATTTATAGAAATGACCTTCCTGAGCCGAGA 1412
QY 6365 GACCAATCTGTTGATTTTGAAGACAGGCAAGCAACACATGTTATTTAGTCCATAGC 6424
Db 1411 GACCAATCTGTTGATTTTGAAGACAGGCAAGCAACACATGTTATTTAGTCCATAGC 1352
QY 6425 CAGGCTCAACAGGGAACAAGTGTGCTTAAACACACAGATGACTGGAATGATGT 6484
Db 1351 CAGGCTCAACAGGGAACAAGTGTGCTTAAACACACAGATGACTGGAATGATGT 1292
QY 6485 GTGGCTCAAGTCCCTGTTCCCAAGATTTTAACTGGAAGAAAGATTGACATTTTGG 6544
Db 1291 GTGGCTCAAGTCCCTGTTCCCAAGATTTTAACTGGAAGAAAGATTGACATTTTGG 1232
QY 6545 CTTAAGAAAAATCGAATGTAGTTTGA 6574

Db 1231 CTTAAGAAAAATCGAATGTAGTTTGA 1202

RESULT 9

US-09-949-016-14275/C
Sequence 14275, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ. ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ. ID NO 14275
LENGTH: 17455
TYPE: DNA
ORGANISM: Human
US-09-949-016-14275

Query Match 8.7%; Score 570; DB 4; Length 17455;
Best Local Similarity 100.0%; Pred. No. 9.3e-151;

Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6005 AGGAGAGAGGCGAGAGTGCCTCTCAAGTTTCACGGTTAACTGTCACCTATTATGACT 6064
Db 15037 AGGAGAGAGGCGAGAGTGCCTCTCAAGTTTCACGGTTAACTGTCACCTATTATGACT 14978
QY 6065 GGAATATAAAGCTGGAACAACCTGCACTGCTGAGATCATCCAGCTGA 6124
Db 14977 GGAATATAAAGCTGGAACAACCTGCACTGCTGAGATCATCCAGCTGA 14918
QY 6125 ATGGAATAATCCGGGACGAGTTGAAAAGTCTGTCGAGAACAGATTATTCGTCGACG 6184
Db 14917 ATGGAATAATCCGGGACGAGTTGAAAAGTCTGTCGAGAACAGATTATTCGTCGACG 14858
QY 6185 AGTTCAATGTAAGTCTGAGACGTGTAATTAATAAATGAGCTTAAGGCTGACAGCCAGC 6244
Db 14857 AGTTCAATGTAAGTCTGAGACGTGTAATTAATAAATGAGCTTAAGGCTGACAGCCAGC 14798
QY 6245 CACCTCTGCTTACAAAAGAGTACTTAGTCACATGACTGTAAAGAAACAATTGTAAACC 6304
Db 14797 CACCTCTGCTTACAAAAGAGTACTTAGTCACATGACTGTAAAGAAACAATTGTAAACC 14738
QY 6305 TCATCTAGAAATCAGAAAGCTTCTAATTTATAGAAATGACCTTCCTGAGCCGAGA 6364
Db 14737 TCATCTAGAAATCAGAAAGCTTCTAATTTATAGAAATGACCTTCCTGAGCCGAGA 14678
QY 6365 GACCAATCTGTTGATTTTGAAGACAGGCAAGCAACACATGTTATTTAGTCCATAGC 6424
Db 14677 GACCAATCTGTTGATTTTGAAGACAGGCAAGCAACACATGTTATTTAGTCCATAGC 14618
QY 6425 CAGGCTCAACAGGGAACAAGTGTGCTTAAACACACAGATGACTGGAATGATGT 6484
Db 14617 CAGGCTCAACAGGGAACAAGTGTGCTTAAACACACAGATGACTGGAATGATGT 14558
QY 6485 GTGGCTCAAGTCCCTGTTCCCAAGATTTTAACTGGAAGAAAGATTGACATTTTGG 6544
Db 14557 GTGGCTCAAGTCCCTGTTCCCAAGATTTTAACTGGAAGAAAGATTGACATTTTGG 14498
QY 6545 CTTAAGAAAAATCGAATGTAGTTTGA 6574
Db 14497 CTTAAGAAAAATCGAATGTAGTTTGA 14468


```
RESULT 10
US-09-513-999C-29836/C
; Sequence 29836, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.Y.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 29836
; LENGTH: 398
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 119
; OTHER INFORMATION: m=a or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 121
; OTHER INFORMATION: w=a or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 124
; OTHER INFORMATION: w=a or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 125
; OTHER INFORMATION: w=a or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 130
; OTHER INFORMATION: w=a or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 136
; OTHER INFORMATION: h=a or c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 138
; OTHER INFORMATION: s=g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 252
; OTHER INFORMATION: s=g or c
US-09-513-999C-29836

Query Match
Best Local Similarity 5.7%; Score 373.2; DB 4; Length 398;
Matches 384; Conservative 7; Mismatches 5; Indels 2; Gaps 1;

QY 6138 GCAGCAGGTTGAAAGTCTGTTCTGAGAACAGATTATTGAGAGAGTTCACTGAGT 6197
DB 398 GCAGCAGGTTGAAAGTCTGTTCTGAGAACAGATTATTGAGAGAGTTCACTGAGT 339
QY 6198 TCTAGACGTGTGACTTAAAGTCTGTTAGGCTGAGAGCCAGCCACTGCTTAC 6257
DB 338 TCTAGACGTGTGACTTAAAGTCTGTTAGGCTGAGAGCCAGCCACTGCTTAC 279
QY 6258 AAAAGAGTACTTACTGACAGTGTGAAGAAACAATTGTTAAACCTCATCTGAATC 6317
DB 278 AAAAGAGTACTTACTGACAGTGTGAAGAAACAATTGTTAAACCTCATCTGAATC 219
QY 6318 AGAAGCTTCTAATTCTATAGAAATGACACCTCCCTGAGCCGAGAGCAATCTGTTGT 6377
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DB 218 AGAAGCTTCTAATTCTATAGAAATGACACCTCCCTGAGCCGAGAGCAATCTGTTGT 159
QY 6378 TGATTTTGAAGACAGGCAAG--ACCAACACTGTATTGTTCCATGCGAGGCTCAAC 6435
DB 158 TGATTTTGAAGACAGGCAAGSADCCACACCTGMMTTWAKTTCATAGCGAGGCTCAAC 99
QY 6436 AGGACAAGTGGCTGGCTTAAAGAACACAGATGACTGAAATGATGTGGCTCAGT 6495
DB 98 AGGACAAGTGGCTGGCTTAAAGAACACAGATGACTGAAATGATGTGGCTCAGT 39
QY 6496 CCTGTTTCCAGAAATTTTACGGAAGAGTTGCA 6533
DB 38 CCTGTTTCCAGAAATTTTACGGAAGAGTTGCA 1

RESULT 11
US-09-016-434-513
; Sequence 513, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSER: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 513:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 258 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAINON01
; CLONE: 2290031
US-09-016-434-513

Query Match
Best Local Similarity 3.9%; Score 258; DB 4; Length 258;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5069 GCAAAGTCGTCATCTCCGCTACAGAAACCTGAGCAAAATCTGCAATCCGAAAGAG 5128
DB 1 GCAAAGTCGTCATCTCCGCTACAGAAACCTGAGCAAAATCTGCAATCCGAAAGAG 60
QY 5129 TAAGACCTGAGAGCCCTGAGCTGTATCACTTCACCAATTAAGATATCTTATGGAA 5188
```

Db 61 TAGAGACTCAGACCCCTGAGCTGTATCCATTCACCAATTAAGATGATTCATTTGAA 120
Qy 5189 CCAATTAATTTCTACGAAATTCGACATGAGACATGACAGCTCGGAGAAATTCCTGGATTAAG 5248
Db 121 CCAATTAATTTCTACGAAATTCGACATGAGACATGACAGCTCGGAGAAATTCCTGGATTAAG 180
Qy 5249 ATGACCATTCCTTGGACAGCTGTGTGTTGCGGCTCTTCGACAGATTCCTGCTGCA 5308
Db 181 ATGACCATTCCTTGGACAGCTGTGTGTTGCGGCTCTTCGACAGATTCCTGCTGCA 240
Qy 5309 TCGTGAGGTGAACAGCG 5326
Db 241 TCGTGAGGTGAACAGCG 258
RESULT 12
US-09-949-016-2640
; Sequence 2640, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VERTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2640
; LENGTH: 2423
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-2640
Query Match 3.5%; Score 228.2; DB 4; Length 2423;
Best Local Similarity 52.2%; Pred. No. 8.9e-54;
Matches 587; Conservative 0; Mismatches 523; Indels 15; Gaps 3;
Qy 170 TATTAGATCCCTCTTGTCTCTTGTGAAGATGACGACGCTGCTGTGATGAATTA 229
Db 1021 TACTGATATACCATCTCCCTTATGATGAATGCAATATCTCCATGAGAGAGAGA 1080
Qy 230 AGCAGGTGAGCACTTGTCCGGAATATCCGACACCAATAGCTGATACAGAGCTCC 289
Db 1081 AGAATCTTCTCGAATACCTAAGATGAGGCTAAACCATTTACTTAAAGTGAACAAATGC 1140
Qy 290 AGCCTTCGCGAAGAGCTTGAAGTGAAGTCTTGTAGGTGTGCTCACTTTGCTGAAG 349
Db 1141 GATTCATAGAGAGAGCTTGAATATTAAGTGATGTGCTGAGAGAGCTTTGGGAGG 1200
Qy 350 TCGAGGTGTAAG 409
Db 1201 TGTGCTAGTAAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
Qy 410 AGGCTTATTTGGCCGAG 469
Db 1261 GGAATATGCTGAAG 1320
Qy 470 GAAGCAAG 529
Db 1321 ATGAG 1380
Qy 530 ATCTGATGAG 589
Db 1381 ACCTGCTTATGAG 1440
Qy 590 ACCAGTTAATGAG 649

Db 1441 ATAGATGCTGAAGATATGCTAGATTTTACTTGGCTGAGATGAGATGAGATTTGACT 1500
Qy 650 GCGTTCATGTATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 709
Db 1501 CAGTTCATGCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1560
Qy 710 GAG 769
Db 1561 TGAATGAG 1620
Qy 770 TGTGATGAG 829
Db 1621 CGGTTCATGCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1680
Qy 830 TGAATGAG 889
Db 1681 CCATGAG 1737
Qy 890 TGAATGAG 949
Db 1738 TGTGATGAG 1797
Qy 950 CCTGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1006
Db 1798 CATAG 1857
Qy 1007 TGAG 1064
Db 1858 TGTGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1917
Qy 1065 -----GAGTTGAG 1117
Db 1918 GTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1977
Qy 1118 ACATTCGATACCTCTCCCT 1177
Db 1978 ATATTCGAG 2037
Qy 1178 ATTTGATGAG 1237
Db 2038 ATTTGATGAG 2097
Qy 1238 CAGGCTTCGAG 1282
Db 2098 CTGCAATTCGAG 2142
RESULT 13
US-08-422-699A-12
; Sequence 12, Application US/08422699A
; Patent No. 5955265
; GENERAL INFORMATION:
; APPLICANT: Brook, J. David
; APPLICANT: Housman, David E.
; APPLICANT: Shaw, Duncan J.
; APPLICANT: Harley, Helen G.
; APPLICANT: Johnson, Keith J.
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
; DYSTROPHY GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,699A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/422,706
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612
FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/839,255
FILING DATE: 20-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB9202485.0
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5830A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2726 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-422-699A-12

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Query Match 3.4%; Score 220.8; DB 2; Length 2726;
Best Local Similarity 53.7%; Pred. No. 1.3e-51;
Matches 531; Conservative 0; Mismatches 442; Indels 15; Gaps 3;

QY 212 CTGCTCTGTAAGATTAGACGCTGAGCACTTTGTCGGAAGTATTCGACACCATATG 271
DB 243 CCGAATCTGGCCAGAGCAAGTACGTGGCCGACTTCTTGAGTGGCGAGCCCATCTG 302
QY 272 CTGAGTTACAGAGCTCCAGCCTTGGCGCAAGAGACTTGAAGTCAAGTCTTGAAGTT 331
DB 303 TGAAGCTTAAGAGAGCTCCAGCTGCGAGAGGAGCACTTCAAGTCTGAAAGTGAATG 362
QY 332 GTGCTCACTTGTCTGAAGTGAAGTGTGAAGAGAAAGCAACCGGGGACATCTATGCTA 391
DB 363 GCGGGGCGTTCAGCAGGAGTACGAGTGAAGATGAAAGAGAGAGCGGGCCAGTGTATG 422
QY 392 TGAAGTGAAGAGAGAGGCTTATTTATGCGCCAGAGAGAGGTTTCAATTTTGAAGAG 451
DB 423 TGAAGTCACTGAACAAGTGGAGCATGCTGAAGAGGGCGAGGTGTCTGCTCCGTGAGG 482
QY 452 AGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCAATTAAGATGCTTTC 511
DB 483 AGAGGAGCGTGTGGTGAATGGGAGCCGCGGTGATCAGCAGCTGCACTTGGCTTCC 542
QY 512 AGGACAAAATACCTTTATCTGATGAGAAATATCACTGAGAGGAGCTTGTCTGAC 571
DB 543 AGGATGAAGAACTACCTGATCCTGATCATGAGTATTAAGTGGGCGGGGACCTGCTGAC 602
QY 572 TTTTGAATAGATATGAGGCGCAGTAGATGAAGAAACCTGATACAGTTTAACTAGTGAGC 631
DB 603 TGCTGAGCAAGTTGGGAGCGGATTCGCGCGAAGATGCGCGCTTCACTGAGGAGGA 662
QY 632 TGAATTTGGCTTTCACAGCGCTTCACTGATGAGGATACGTGCATGAGACATCAAGCCTG 691
DB 663 TTGTCATGCGCATATGACTCGGTGACCGGCTTGGCTTACGTGACAGGAGCATCAAAACCG 722

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QY 692 AAGAACTTCTGTTAGCCGACAGACATCAAGCTGTGTGATTTGGATCTGCGCGCA 751
DB 723 ACAACATCTCTGAGACCGCTGTGGCCACATCTGCGCTGGCCGACTTGGCTTGCCTCA 782
QY 752 AATGAAATTCAAACAAGATGTGAATGCAACTCCGATTTGGAGCCCCAGATTACATGG 811
DB 783 AGCTGGGGCAGATGAACGAGTGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 842
QY 812 CTCTGAAGTGTCTGA---CTGTATGAAGAGGAGATGAAGAAAGGACCTAGGCTGAGCT 868
DB 843 CCCCCGAGATCTGTGAGGCTGTGTGGCGGTGTGGCGCTGAGACAGAGCTACGAGCCGAGT 902
QY 869 GTGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 928
DB 903 GTGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 962
QY 929 CAGAGGAACCTCTGCGCAAGACCTTCATTAATTAATTAATTAATTAATTAATTAATTA 988
DB 963 AGCGGAATTCACGCGGAGACCTATGAGCAAGATCTCACTACAAAGAGACCTCTCTC 1022
QY 989 TTCCAGATGACCCCAAGTGAAGCACT---GACTTCTGTATCTGATTCGAAGCTTGTGT 1045
DB 1023 TGCCGCTGTGTGAGAGAGGAGTCCCTGAGAGGCTCGAGACTTCACTTACGCGGTGTGT 1082
QY 1046 GCGGCTCAAAAGAGAGACTGAAGTTGAAGTCTTTGTCTG-----CATCTTTCT 1096
DB 1083 GTCCCCCGGAGACACGCTGTGGCGCGGTGTGAGAGCGGACTTCCGACACATCTCTCT 1142
QY 1097 TCTTAAATTAATGACTGGAACAACATTCGTACTCTCCCTCCCTGTGTGTCACCCCTCA 1156
DB 1143 TCTTTGGCTGTGACTGTGGATGTGTCTCGGAGACAGCTGCCCCCTTTACACGGAATTCG 1202
QY 1157 AGTCTGACATGACACTCTCAATTTTGA 1184
DB 1203 AAGGTGCCACCGACACATGCAACTTGA 1230

```

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RESULT 14
US-08-422-706B-12
Sequence 12, Application US/08422706B
GENERAL INFORMATION:
PATENT NO. 5977333
APPLICANT: Brook, J. David
APPLICANT: Houseman, David E.
APPLICANT: Shaw, Duncan J.
APPLICANT: Harley, Helen J.
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02713
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,706B
FILING DATE: 14-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/284,543
FILING DATE: 08-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612
FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:

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/ ATTORNEY/AGENT INFORMATION:
/ NAME: Granahan, Patricia
/ REGISTRATION NUMBER: 32,227
/ REFERENCE/DOCKET NUMBER: MIT-5830A2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-861-6240
/ TELEFAX: 617-861-9540
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2511 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..1746
/ US-08-422-699A-8
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Query Match 3.3%; Score 214; DB 2; Length 2511;
Best Local Similarity 54.2%; Pred. No. 1e-49;
Matches 508; Conservative 0; Mismatches 415; Indels 15; Gaps 3;
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DB 103 GTGATCGAGCGGGGGCGTTCAAGCGGTAGCGGTAGTGAAGATGAAGACAGCGGGCCAG 162
QY 382 ATCTATGCTATGAAAGTGTATGAAGAAGAGCGCTTTATGGCCAGAGCAGGTTTCATT 441
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QY 562 TTGCTGTCACTTTTGAATGATATGAGACACAGTTAGTGAATAACCTGATACAGTTTAC 621
DB 343 CTGCTGACACTGCTGAGCAAGTTGGGGAGCGGATTCGGCCGAGATGCGCGCTTCTAC 402
QY 622 CTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCACTGATGAGATACGTGATCGAGAC 681
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DB 463 ATCAAAACCGAACAATCTGCTGAGACGCTGTGGCCACATCCGCTGTGCCGACTTCGGC 522
QY 742 TCTGCCGCAAAATGATTAACAAGATGTGAATGCCAACTCCCGATTGGACCCCA 801
DB 523 TCTTGCTCAAGCTGCGGCAATGAAAGGTGCGGTGCTGTGGCTGTGGCAACCCA 582
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Job time : 962.599 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2005, 10:30:48 ; Search time 893.401 Seconds
(without alignments)
11280.299 Million cell updates/sec

Title: US-10-017-216-3

Perfect score: 6159
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5661.4	91.9	6165	4 US-10-028-946-1	Sequence 1, App11
2	5358	87.0	5877	4 US-10-028-946-3	Sequence 3, App11
3	1391.8	22.6	1515	4 US-09-804-471A-1	Sequence 1, App11
4	1391.8	22.6	1515	4 US-10-238-709-1	Sequence 1, App11
5	952.4	15.5	2162	4 US-09-774-528-419	Sequence 419, App
6	750	12.2	1133	4 US-09-916-204-1	Sequence 1, App11
7	750	12.2	1133	4 US-10-282-048-1	Sequence 1, App11
8	258	4.2	258	4 US-09-016-434-513	Sequence 513, App
9	228.2	3.7	2423	4 US-09-949-016-2640	Sequence 2640, App
10	220.8	3.6	2726	4 US-08-422-699A-12	Sequence 12, App1
11	220.8	3.6	2726	4 US-08-422-706B-12	Sequence 12, App1
12	214	3.5	2511	2 US-08-422-699A-8	Sequence 8, App11
13	214	3.5	2511	2 US-08-422-706B-8	Sequence 8, App11
14	213.6	3.5	3182	4 US-08-484-044-11	Sequence 11, App1
15	205	3.3	174493	4 US-09-804-471A-3	Sequence 3, App11
16	205	3.3	174493	4 US-10-238-709-3	Sequence 3, App11
17	189.2	3.1	2706	2 US-08-630-822A-61	Sequence 61, App1
18	189.2	3.1	2706	2 US-09-005-069-61	Sequence 61, App1
19	189.2	3.1	2706	4 US-09-171-156A-20	Sequence 20, App1
20	189.2	3.1	2706	4 US-09-004-730A-20	Sequence 20, App1
21	189.2	3.1	2706	4 US-08-981-799A-20	Sequence 20, App1
22	181.2	2.9	4363	2 US-08-685-576-5	Sequence 295, App
23	179.6	2.9	4888	4 US-09-976-594-295	Sequence 295, App
24	178.8	2.9	48763	4 US-09-916-204-3	Sequence 3, App11
25	178.8	2.9	48763	4 US-10-282-048-3	Sequence 3, App11
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27	173	2.8	2188	4 US-09-949-016-2533	Sequence 2533, Ap

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	29	172.2	2.8	4065	3 US-09-016-434-1105	Sequence 1105, Ap
	30	172.2	2.8	4739	2 US-08-685-871-1	Sequence 1, App11
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	35	122.6	2.0	3155	4 US-08-939-106-7	Sequence 7, App11
	36	122.6	2.0	3155	4 US-09-442-102-7	Sequence 7, App11
	37	122.2	2.0	1998	3 US-09-509-902A-6	Sequence 6, App11
	38	122.2	2.0	1961	3 US-09-509-902A-15	Sequence 15, App1
	39	122.2	2.0	5276	4 US-09-233-857-2	Sequence 2, App11
	40	117.8	1.9	3018	2 US-08-860-150-6	Sequence 6, App11
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	42	111.4	1.8	1935	2 US-08-878-989-11	Sequence 11, App1
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	45	109.8	1.8	3213	4 US-08-939-106-5	Sequence 5, App11

ALIGNMENTS

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32
1440

RESULT 1
US-10-028-946-1
Sequence 1, Application US/10028946
Patent No. 6734009
GENERAL INFORMATION:
APPLICANT: Yu, Xuanchuan
APPLICANT: Miranda, Maricar
APPLICANT: Fiddler, Carl Johan
TITLE OF INVENTION: NO. 6734009 Human Kinases and Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0289-USA
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US/10/028,946
PRIOR FILING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 6165
TYPE: DNA
ORGANISM: homo sapiens
US-10-028-946-1

Query Match 91.9%; Score 5661.4; DB 4; Length 6165;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 5944; Conservative 16; Indels 243; Gaps 3;

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DB	61	GCACGCGCGGCTCCAGGCTGAATCTTCCAGGGGAAACCAACCCCTTATGACTCA	120
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DB	121	CAGCAGATGTCCTCTTCCGAGAAAGATATTAATGCCCCCTTTGTTCTTTGAA	180
QY	181	GAATGATGTCAGCTGCTCTGATGAATTAAGCACTGAGCAACTTTGTCGGAAGT	240
DB	181	GAATGATGTCAGCTGCTCTGATGAATTAAGCACTGAGCAACTTTGTCGGAAGT	240
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DB	241	TCCGACACCATGCTGATTAAGAGCTCCAGCTTGCGGCAAGAGACTTGAAGTCA	300
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Db 2401 ATTCTGAGGAAACAGAAAGGCGATGATCAATGATGATGATGATGATGATGATGATGATGAT 2460
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Qy 3733 CAACCAAACTCATTTGATTTTCTGCAAGCCAAATGACCAACTGCTTAAAAAGAAAG 3792
Db 3781 CAACCAAACTCATTTGATTTTCTGCAAGCCAAATGACCAACTGCTTAAAAAGAAAG -- 3838
Qy 3793 GGTATTATTTAGTCAGAGAAAGAGACCTCGTTTACCACACAGGTTCTCTGAGTAC 3852
Db 3839 -----AGGTTCTCTGAGTAC 3855
Qy 3853 AATGAGCTGAAGCTGGCCCTGAGAGAAAGAAAGCTCGCTGTGACAGCTTAGAGAGAGCC 3912
Db 3856 AATGAGCTGAAGCTGGCCCTGAGAGAAAGAAAGCTCGCTGTGAGAGCTTAGAGAGAGCC 3915
Qy 3913 CTTTCAAGAGACCCGATGAGGCTCCGCTCCGCGAGAGAAAGTCCCAACGCAAGCA 3972
Db 3916 CTTTCAAGAGACCCGATGAGGCTCCGCTCCGCGAGAGAAAGTCCCAACGCAAGCA 3975
Qy 3973 AAGGACCAACCCACACCATCCAGCCAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4032
Db 3976 AAGGACCAACCCACACCATCCAGCCAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4035
Qy 4033 ATCTGCGGTCGCGCAGAGAGCAGGCGAGTGCATGAGGCTGTGAGCCCGGCAATCAGC 4092
Db 4036 ATCTGCGGTCGCGCAGAGAGCAGGCGAGTGCATGAGGCTGTGAGCCCGGCAATCAGC 4095
Qy 4093 CGCAGAAAGAGTCTTCAACTCAGAGAAATTTAGTCCGCTCTTAAGGAACGATGCAC 4152
Db 4096 CGCAGAAAGAGTCTTCAACTCAGAGAAATTTAGTCCGCTCTTAAGGAACGATGCAC 4155
Qy 4153 CACAAATTTCTCACCAGATTCAAAGTGAAGCTGAACATGCGAGCCACAAAGTGTGTCG 4212
Db 4156 CACAAATTTCTCACCAGATTCAAAGTGAAGCTGAACATGCGAGCCACAAAGTGTGTCG 4215
Qy 4213 TGTCTGATACCGTGCATTTGGAAGCGCAGGATCCAAATGTCTGAAATGTGAGGTATG 4272
Db 4216 TGTCTGATACCGTGCATTTGGAAGCGCAGGATCCAAATGTCTGAAATGTGAGGTATG 4275
Qy 4273 TGTCAACCCCAAGTGTCCACGTTGCTTGCAGGCACTGCGGCTTGCCTGAATATGCC 4332
Db 4276 TGTCAACCCCAAGTGTCCACGTTGCTTGCAGGCACTGCGGCTTGCCTGAATATGCC 4335
Qy 4333 ACACACTTCAACGAGAGGCTTCTGCGGTGACAAATGAACTCCCGAGGTCTCCAGACCAAG 4392
Db 4336 ACACACTTCAACGAGAGGCTTCTGCGGTGACAAATGAACTCCCGAGGTCTCCAGACCAAG 4395
Qy 4393 GAGCCAGCAGAGCTTGCACCTGGAAGGAGTGAAGTGAAGTCCAGAAATTAACAAACGA 4452
Db 4396 GAGCCAGCAGAGCTTGCACCTGGAAGGAGTGAAGTGAAGTCCAGAAATTAACAAACGA 4455
Qy 4453 GGAACGCAAGGCTGGAGACAGAAATGATTTGCTTGAAGAGATCAAAAGTCTCATTTAT 4512
Db 4456 GGAACGCAAGGCTGGAGACAGAAATGATTTGCTTGAAGAGATCAAAAGTCTCATTTAT 4515
Qy 4513 GACAAATGAAGCCAGAGAGTGAACAGAGCCGAGTGAAGAAATTTGAGTGTGCTTCCC 4572
Db 4516 GACAAATGAAGCCAGAGAGTGAACAGAGCCGAGTGAAGAAATTTGAGTGTGCTTCCC 4575
Qy 4573 GACGGGATGTATTAATCATAGTGCCTGTTGCTTCCGAATCTGCAAAATACAGCAAA 4632
Db 4576 GACGGGATGTATTAATCATAGTGCCTGTTGCTTCCGAATCTGCAAAATACAGCAAA 4635
Qy 4633 GCA----- 4635
Db 4636 GCAGATGTCCATACATACTGAAGATGAATCTCACCCGACACACACTGTGCCCCGG 4695

QY	4636	-----	4635
Db	4696	AGAACCTCTACTGTGTAGCTCCAGCTTCCCTGACAAACAGCGTGGGTGACCGCTTA	4755
QY	4696	-----	4662
Db	4756	GAATCACTTTCGCAAGTGGGAGATTCTAGGGAAAAAGCAAGAGCTGATGCTTAACCTG	4815
QY	4663	CTTGGAAACTCCCTGTCTGAAACTGGAAGGTGATGACCGTCTAGACATGCAACGCTG	4722
Db	4816	CTTGGAAACTCCCTGTCTGAAACTGGAAGGTGATGACCGTCTAGACATGCAACGCTG	4875
QY	4723	CCCTTCAATGACCAAGTGTGTGTGGTGGGACCCAGGAAGGGCTTACGCCCTGATATTC	4782
Db	4876	CCCTTCAATGACCAAGTGTGTGTGGTGGGACCCAGGAAGGGCTTACGCCCTGATATTC	4935
QY	4783	TTGAAAAAATCCCTTAACCATATGTCCACGAAATTGGAGAGCTTCCAAATTATATATTC	4842
Db	4936	TTGAAAAAATCCCTTAACCATATGTCCACGAAATTGGAGAGCTTCTCAAAATTATATATTC	4995
QY	4843	AAGGACCTGAGAAAGCTTACATGATAGACAGAGAGACGGGACATGTGTCTTGTGGAC	4902
Db	4996	AAGGACCTGAGAAAGCTTACATGATAGACAGAGAGAGACGGGACATGTGTCTTGTGGAC	5055
QY	4993	GTGAAGAAAGTGAACAGTCCCTGGCCCAAGTCCCACTGCTGCTGCCACGCCGACATCTCA	4962
Db	5056	GTGAAGAAAGTGAACAGTCCCTGGCCCAAGTCCCACTGCTGCTGCCACGCCGACATCTCA	5115
QY	4963	CCCAACATTTTGTGAAGCTGTACAGAGGGCTGCCACTGTTTGGGGGACGAAATTTGAGAC	5022
Db	5116	CCCAACATTTTGTGAAGCTGTACAGAGGGCTGCCACTGTTTGGGGGACGCAATTTGAGAC	5175
QY	5023	GGGCTCTGTCATCTGTGCAGCCATGCGCCAGCAAGTGTGATTTCTCCGCTACAGAAAC	5082
Db	5176	GGGCTCTGTCATCTGTGCAGCCATGCGCCAGCAAGTGTGATTTCTCCGCTACAGAAAC	5235
QY	5083	CTCAGCAAAATCTGCATCCGGAAGAGATAGACCTCAGAGCCCTGACCTGTATCCAC	5142
Db	5236	CTCAGCAAAATCTGCATCCGGAAGAGATAGACCTCAGAGCCCTGACCTGTATCCAC	5295
QY	5143	TTCAACCAATTCAGATTCCTCATTTGGAAACCAATTAATTCAGAAATTCAGATAGAGAG	5202
Db	5296	TTCAACCAATTCAGATTCCTCATTTGGAAACCAATTAATTCAGAAATTCAGATAGAGAG	5355
QY	5203	TACACGCTCGAAGAAATCTTGATAGATAGACCATTCCTTGGGACACCTGTGTGTTGCC	5262
Db	5356	TACACGCTCGAAGAAATCTTGATAGATAGACCATTCCTTGGGACACCTGTGTGTTGCC	5415
QY	5263	GCCCTCTTCCACACACTTCCCTGTCTCAATCTGTGCAGGTGAACAGCGCACGCGAGAG	5322
Db	5416	GCCCTCTTCCACACACTTCCCTGTCTCAATCTGTGCAGGTGAACAGCGCACGCGAGAG	5475
QY	5323	GAGTACTTGCATGTGTTTCCAGAAATTGGAAATGTTCGTGATTTCTTACGGAAGACGTAGC	5382
Db	5476	GAGTACTTGCATGTGTTTCCAGAAATTGGAAATGTTCGTGATTTCTTACGGAAGACGTAGC	5535
QY	5383	CGCACAGACGATCTCAAGTGAAGTGCCTTACCTTGGGCTTGTGCTACAGAGAACCTTAT	5442
Db	5536	CGCACAGACGATCTCAAGTGAAGTGCCTTACCTTGGGCTTGTGCTACAGAGAACCTTAT	5595
QY	5443	CTGTTTTGTGACCCACTTCAACTCACTGGAATTAATGATATCAGGACCGCTCTCTACGA	5502
Db	5596	CTGTTTTGTGACCCACTTCAACTCACTGGAATTAATGATATCAGGACCGCTCTCTACGA	5655
QY	5503	GGGACCCCTGCGAGAGGTACCTGAGACATCCGAAACCGCGCTACCTGGGCTCTGCATT	5562
Db	5656	GGGACCCCTGCGAGAGGTACCTGAGACATCCGAAACCGCGCTACCTGGGCTCTGCATT	5715
QY	5563	TCTCAGAGAGCATTTTACTTGGGCTCTCATATACAGAGATAATTAAGGGTCAATTGGCTGC	5622
Db	5716	TCTCAGAGAGCATTTTACTTGGGCTCTCATATACAGAGATAATTAAGGGTCAATTGGCTGC	5775
QY	5623	AAGGAAAATCTCGTGAAGAGTCCGGGACCTGAAACACACCGGGGCTCGTCACTTCCGC	5682

Dd	5776	AAGGAAACCTCGTGAAGGAGTCGGGCATCGAACCAACCCGGGCCGTCTCACCTCCGC	5835
Oy	5683	AGCAGCCCACAAGCAGCAGAGGCCAACCACGNTACAAACAGACATCACCAAAGCGTGACC	5742
Dd	5836	AGCAGCCCCAACAAAGCAGAGGCCCAACCGTAACAGACATCATCCAAGCGGTGACC	5895
Oy	5743	TCCAGCCCAAGCGCCGCCGAAGGCCCAAGCCACCCCGAGAGGCCAACACACCCCAACGC	5802
Dd	5896	TCCAGCCCAAGCGCCGCCGAAGGCCCAAGCCACCCCGAGAGGCCAACACACCCCAACGC	5955
Oy	5803	TACCGCCCAAGCGCCGCCGAAGGCCCAAGCCACCCCGAGAGGCCAACACACCCCAACGC	5862
Dd	5956	TACCGCCCAAGCGCCGCCGAAGGCCCAAGCCACCCCGAGAGGCCAACACACCCCAACGC	6015
Oy	5863	GAGAAGTCCCCCGGCGGATGCTCAGACACCGAGAGAGCGGTCCCCCGGAGAGCTGTT	5922
Dd	6016	GAGAAATCCCCCGGCGGATGCTCAGACACCGAGAGAGCGGTCCCCCGGAGAGCTGTT	6075
Oy	5923	GAAAGCAGCAGCAGAGGCGCGGCTGCTCGCGAGACCGCTGAGAGACCCCGCTGTCCAGGTG	5982
Dd	6076	GAAAGCAGCAGCAGAGGCGCGGCTGCTCGCGAGACCGCTGAGAGACCCCGCTGTCCAGGTG	6135
Oy	5983	AACAAGGAAAGGAGGCGAGATGC	6005
Dd	6136	AACAAGGTCGTGGACCACTCTC	6158

RESULT 2
US-10-028-946-3
; Sequence 3, Application US/10028946
; Patent No. 6734009
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Mirandea, Maricar
; TITLE OF INVENTION: No. 6734009el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5877
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-028-946-3

Query Match 87.0%; Score 5358; DB 4; Length 5877;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 5634; Conservative 0; Mismatches 5; Indels 243; Gaps 3;

Oy	1	ATGTTGAAGTTCAAAATATGAGCGCGGAATCCTTGGATGCTGTGCTGAAACCAT	60
Dd	1	ATGTTGAAGTTCAAAATATGAGCGCGGAATCCTTGGATGCTGTGCTGAAACCAT	60
Oy	61	GCCAGCGCGGCGCTTCCAGGCTGATCTGTTTTTCCAGGGGAAAACACCCCTTATGACTCAA	120
Dd	61	GCCAGCGCGGCGCTTCCAGGCTGATCTGTTTTTCCAGGGGAAAACACCCCTTATGACTCAA	120
Oy	121	CAGCAGATGCTCCTCTTTCCGAGAAAGGATATTAGATGCCCTTTGTTCTTTGAA	180
Dd	121	CAGCAGATGCTCCTCTTTCCGAGAAAGGATATTAGATGCCCTTTGTTCTTTGAA	180
Oy	181	GAAATGAGTCAAGCTGCTGTGATGAAGATTAAAGCAGTAGCAACTTTGTCCGAAGTAT	240
Dd	181	GAAATGAGTCAAGCTGCTGTGATGAAGATTAAAGCAGTAGCAACTTTGTCCGAAGTAT	240
Oy	241	TCCGACCACTATAGTATGATTACAGAGCTTCAGCTTCCGCAAAAGACTTCCAGTCA	300
Dd	241	TCCGACCACTATAGTATGATTACAGAGCTTCAGCTTCCGCAAAAGACTTCCAGTCA	300

QY 301 AGCTTGTAGGTGTGTGCTGCTGAGTGCAGGTGTAGAGAGAAAGCAACGGG 360
DB 301 AGCTTGTAGGTGTGTGCTGCTGAGTGCAGGTGTAGAGAGAAAGCAACGGG 360
QY 361 GACATCTATGCTATGAAAGTATGAGAGAAAGGCTTATTTGGCCAGAGACAGTTTCA 420
DB 361 GACATCTATGCTATGAAAGTATGAGAGAAAGGCTTATTTGGCCAGAGACAGTTTCA 420
QY 421 TTTTGTGAGAGAGAGGGAACATATTAATCTGAGACAAAGCCCGTGGATCCCCAATTA 480
DB 421 TTTTGTGAGAGAGAGGGAACATATTAATCTGAGACAAAGCCCGTGGATCCCCAATTA 480
QY 481 CAGTAGCCCTTTAGAGACAAATAATCACTTTATCTGATGAGAGAAATTCAGCCTGAGAG 540
DB 481 CAGTAGCCCTTTAGAGACAAATAATCACTTTATCTGATGAGAGAAATTCAGCCTGAGAG 540
QY 541 GACTTGTCTGCTATTTGAAATAGATATGAGAGACAGTTAGATGAAACCTGATACAGTTT 600
DB 541 GACTTGTCTGCTATTTGAAATAGATATGAGAGACAGTTAGATGAAACCTGATACAGTTT 600
QY 601 TA6CTAGCTGAGCTGATTTTGGCTGTTCAAGCGTTTCACTGATGAGGATACGTGATCGA 660
DB 601 TA6CTAGCTGAGCTGATTTTGGCTGTTCAAGCGTTTCACTGATGAGGATACGTGATCGA 660
QY 661 GAGATCAAGCTGAGAGACATTTCTGTTGACCCGACAGAGACATCAAGCTGTGGATTTT 720
DB 661 GAGATCAAGCTGAGAGACATTTCTGTTGACCCGACAGAGACATCAAGCTGTGGATTTT 720
QY 721 GGAATCGCCGGAATAATGAAATCAACAAGATGATGATGCAAACTCCGATTTGGAGAC 780
DB 721 GGAATCGCCGGAATAATGAAATCAACAAGATGATGATGCAAACTCCGATTTGGAGAC 780
QY 781 CCGATTTACATGCTGCTGTAAGTGTGATGATGATGATGATGATGATGATGATGATGATG 840
DB 781 CCGATTTACATGCTGCTGTAAGTGTGATGATGATGATGATGATGATGATGATGATGATG 840
QY 841 GGGCTGAGACTGTGACTGT 900
DB 841 GGGCTGAGACTGTGACTGT 900
QY 901 TCCCTCTGAGAGAGGAACTCTGCGCAGAACCTTCAATTAATTAATTAATTAATTAATTA 960
DB 901 TCCCTCTGAGAGAGGAACTCTGCGCAGAACCTTCAATTAATTAATTAATTAATTAATTA 960
QY 961 TTTTGTGAAATTTTCCAGATGACCCCAAGTGAAGCATTTCTTGTATGATTTCAAGC 1020
DB 961 TTTTGTGAAATTTTCCAGATGACCCCAAGTGAAGCATTTCTTGTATGATTTCAAGC 1020
QY 1021 TTTTGT 1080
DB 1021 TTTTGT 1080
QY 1081 TCTTAAATTTGATGAGAAACATTTGTAATCTCTCTCCCTGTTGTTCCACCTCAAG 1140
DB 1081 TCTTAAATTTGATGAGAAACATTTGTAATCTCTCTCCCTGTTGTTCCACCTCAAG 1140
QY 1141 TCTGAGATGACACTTCAATTTTGTATGAAACAGAGAGAAATCGTGGTTTCACTCTG 1200
DB 1141 TCTGAGATGACACTTCAATTTTGTATGAAACAGAGAGAAATCGTGGTTTCACTCTG 1200
QY 1201 CCGTGTGAGTGTGAGCCCTGAGGCTTCTCGGTGAAAGAACTGCGGTTTGTGGGGTTTGG 1260
DB 1201 CCGTGTGAGTGTGAGCCCTGAGGCTTCTCGGTGAAAGAACTGCGGTTTGTGGGGTTTGG 1260
QY 1261 TACAGCAAGGCACTGGGGATTTTGTGATGATGATGATGATGATGATGATGATGATGATG 1320
DB 1261 TACAGCAAGGCACTGGGGATTTTGTGATGATGATGATGATGATGATGATGATGATGATG 1320
QY 1321 CCTGCAAGACTAGCTTCATGAGAAAGAACTTTCTCATCAAAAGCAAGACTTCAAGAC 1380
DB 1321 CCTGCAAGACTAGCTTCATGAGAAAGAACTTTCTCATCAAAAGCAAGACTTCAAGAC 1380

QY 1381 TCTCAGAGCAAGTGTCACAAGATGAGCAGAAATGACCCGGTTACATCGAGAGTGTCA 1440
DB 1381 TCTCAGAGCAAGTGTCACAAGATGAGCAGAAATGACCCGGTTACATCGAGAGTGTCA 1440
QY 1441 GAGGTGAGGCTGTGTGTTAGTCAAGAGAGGTGAGCTGAGAGGCTTGTAGACTCAGAGA 1500
DB 1441 GAGGTGAGGCTGTGTGTTAGTCAAGAGAGGTGAGCTGAGAGGCTTGTAGACTCAGAGA 1500
QY 1501 TCCCTCTGTGAGACAGGACTTGTCTACATCAACAGAAATGCAAGTATGCAATTAAGCAAT 1560
DB 1501 TCCCTCTGTGAGACAGGACTTGTCTACATCAACAGAAATGCAAGTATGCAATTAAGCAAT 1560
QY 1561 TTGAGCAAGCAAGGATGAGGTGTCCAGAGAGATGACAAAGCACTGAGCTTCCAT 1620
DB 1561 TTGAGCAAGCAAGGATGAGGTGTCCAGAGAGATGACAAAGCACTGAGCTTCCAT 1620
QY 1621 GATATCAGAGACAGAGCCGGAAGCTCCAGAAATCAAGAGCAGAGTACAGGCTCA 1680
DB 1621 GATATCAGAGACAGAGCCGGAAGCTCCAGAAATCAAGAGCAGAGTACAGGCTCA 1680
QY 1681 GTTGAAGAAATGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
DB 1681 GTTGAAGAAATGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
QY 1741 CCGAGTGTCTGTAGGAATCTGAGCTGAGAGAGTCTCGGCTTGTGTAAGATTTCAAG 1800
DB 1741 CCGAGTGTCTGTAGGAATCTGAGCTGAGAGAGTCTCGGCTTGTGTAAGATTTCAAG 1800
QY 1801 CCGAAAGCAGACAGAAATGTGAGATTAATCTTTGAAGCTTAAGATTAAGAGAGCTGGA 1860
DB 1801 CCGAAAGCAGACAGAAATGTGAGATTAATCTTTGAAGCTTAAGATTAAGAGAGCTGGA 1860
QY 1861 GTTGGAGAAATATGCGAAACTGAGAGAAAGATCAATGCTGAGACAGCTCAAAATTCAGAG 1920
DB 1861 GTTGGAGAAATATGCGAAACTGAGAGAAAGATCAATGCTGAGACAGCTCAAAATTCAGAG 1920
QY 1921 CTCGAAGAGAACTGAGAGAGCT----- 1944
DB 1921 CTCGAAGAGAACTGAGAGAGCT----- 1944
QY 1945 -----GCAAGAGAGCAGCCGAGAGAGCTGAGAGAGCTGAGAGAGCTGAGAGAG 1992
DB 1945 -----GCAAGAGAGCAGCCGAGAGAGCTGAGAGAGCTGAGAGAGCTGAGAGAG 1992
QY 1981 AATATCCGCAAGCAAG 2040
DB 1981 AATATCCGCAAGCAAG 2040
QY 1993 GATTTCTTGTGAAGCATCAAGAAAGAGCTGTGTGAAGCTGTGAGAGAGAGAGAGAGAG 2052
DB 1993 GATTTCTTGTGAAGCATCAAGAAAGAGCTGTGTGAAGCTGTGAGAGAGAGAGAGAGAG 2052
QY 2041 GATTTCTTGTGAAGCATCAAGAAAGAGCTGTGTGAAGAGAGAGAGAGAGAGAGAGAG 2100
DB 2041 GATTTCTTGTGAAGCATCAAGAAAGAGCTGTGTGAAGAGAGAGAGAGAGAGAGAGAG 2100
QY 2053 GAGAACAGGTAAAGAGCTAGAGCAATGAGAGCTTGAAGAAAGAGAGAGAGAGAGAG 2112
DB 2053 GAGAACAGGTAAAGAGCTAGAGCAATGAGAGCTTGAAGAAAGAGAGAGAGAGAGAGAG 2112
QY 2101 GAGAACAGGTAAAGAGCTAGAGCAATGAGAGCTTGAAGAAAGAGAGAGAGAGAGAG 2160
DB 2101 GAGAACAGGTAAAGAGCTAGAGCAATGAGAGCTTGAAGAAAGAGAGAGAGAGAGAG 2160
QY 2113 ATTCAGACAAATTCACACAGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2172
DB 2113 ATTCAGACAAATTCACACAGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2172
QY 2161 ATTCAGACAAATTCACACAGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
DB 2161 ATTCAGACAAATTCACACAGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
QY 2173 AAACATCGGAGAGCCCAAGTCTCAGCCAGCAGCTTGAAGAGAGAGAGAGAGAGAGAG 2232
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QY 2221 AAACATCGGAGAGCCCAAGTCTCAGCCAGCAGCTTGAAGAGAGAGAGAGAGAGAGAG 2280
DB 2221 AAACATCGGAGAGCCCAAGTCTCAGCCAGCAGCTTGAAGAGAGAGAGAGAGAGAGAG 2280
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DB 2233 CAGCACTATGAGAGAAAGATTAAGTGTGCAATCGATTAAGAGAGAGAGAGAGAGAGAG 2292
QY 2281 CAGCACTATGAGAGAAAGATTAAGTGTGCAATCGATTAAGAGAGAGAGAGAGAGAGAG 2340
DB 2281 CAGCACTATGAGAGAAAGATTAAGTGTGCAATCGATTAAGAGAGAGAGAGAGAGAGAG 2340
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QY 2341 AAGGAGACACTGAGAGACATGATGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
DB 2341 AAGGAGACACTGAGAGACATGATGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
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DB 2353 ATTCTAGGAGACAGAGAGAGATGATCAATGCTTATGATTTCAAGATCAGATCCTGGAA 2412
QY 2401 ATTCTAGGAGACAGAGAGAGATGATCAATGCTTATGATTTCAAGATCAGATCCTGGAA 2460
DB 2401 ATTCTAGGAGACAGAGAGAGATGATCAATGCTTATGATTTCAAGATCAGATCCTGGAA 2460
QY 2413 CAGAGATTTGTGAACTGTCTAGAGCAATAAATTTGAGCAAGAAATGAGAGTCTTTTACC 2472
DB 2413 CAGAGATTTGTGAACTGTCTAGAGCAATAAATTTGAGCAAGAAATGAGAGTCTTTTACC 2472

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Db 2521 CAAAGGAACATGAAGGCCAAAGAAAGATGATTTCTGAACCTCAGCAACAGAAATTTTAC 2580
Qy 2533 CTGAGACACACAGCTGGGAAGTTGGAGGCCAGAACCGAAATCTGGAGAGCAAGCTGGAG 2592
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Qy 2653 CGGAGGTCAGTCTAGAGCAAGAGAGCAGAAATCTGAAGCTCAAAGGCCAGCTCACAGAG 2712
Db 2701 CGGAGGTCAGTCTAGAGCAAGAGAGCAGAAATCTGAAGCTCAAAGGCCAGCTCACAGAG 2760
Qy 2713 CTACAGCTCTCCCTGACAGAGCCGAGTCAAGTTGACAGCCCTGACAGGCTGACAGGGCG 2772
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Qy 2773 GCCCTGAGAGCCAGCTTCCGACAGCGAAGACAGAGCTGGAAGAGACCAAGCAAGAGCT 2832
Db 2821 GCCCTGAGAGCCAGCTTCCGACAGCGAAGACAGAGCTGGAAGAGACCAAGCAAGAGCT 2880
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Qy 2893 CTTCTGTAACAGCTGTACTGTAAATCAGACCTGGAGAGACAGCTAAACAGCTGACCGAG 2952
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Qy 2953 GACAAAGCTGAACTCAACAAACCAAACTTCTACTTTCCAAACAACTCGATAGGCTTCT 3012
Db 3001 GACAAAGCTGAACTCAACAAACCAAACTTCTACTTTCCAAACAACTCGATAGGCTTCT 3060
Qy 3013 GGGCGCAACGACGAGATTGTACAACTGCGAAGTGAAGTGAACATCTCCGCGGAGATC 3072
Db 3061 GGGCGCAACGACGAGATTGTACAACTGCGAAGTGAAGTGAACATCTCCGCGGAGATC 3120
Qy 3073 ACGGAACGAGAGATGACGCTTACAGCCAGAAAGCAAAACGATGAGGCTTGAAGACAG 3132
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Qy 3133 TGCACCATGCTGAGAGAACAGGTCAATGATTGGAGGCCCTTAACAGATGAGCTGCTAAGA 3192
Db 3181 TGCACCATGCTGAGAGAACAGGTCAATGATTGGAGGCCCTTAACAGATGAGCTGCTAAGA 3240
Qy 3193 AAAAGACGCGACGTGGAGGCCCTGAGAGACGTCCTGGGTGATGAAGAAATCCAGTTTGA 3252
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Qy 3253 TGTGGGGTTCCGAGACTGAGAGAAATGCTGACACCGAGAAACAGAGCGGCGAGAGCC 3312
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Qy 3373 GAGATTTCTGCTCTGACAGAGGCTTCAAAGACAGAAAGCTGAAGGCCGAGAGGCTCTCT 3432
Db 3421 GAGATTTCTGCTCTGACAGAGGCTTCAAAGACAGAAAGCTGAAGGCCGAGAGGCTCTCT 3480
Qy 3433 GACAAGCTCAATGACCTGAGAGAAAGCATGCTAATGCTTGAATGAATGCCGAAGCTTA 3492
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Qy 3493 CAGCAGAAAGCTGAGACTGAACGAGAGCTCAACAGAGGCTTCTGGAAGAGCAAGCCAA 3552
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Qy 3553 TTAACAGCAGAGATGGAACCTGACAGAAAATGACATTTTCCGCTTACATCTCAAGATCTGCA 3612
Db 3601 TTAACAGCAGAGATGGAACCTGACAGAAAATGACATTTTCCGCTTACATCTCAAGATCTGCA 3660
Qy 3613 GAACTCTAAGATCGGCTGATCTACTGAAGACAGAAAGAGTCACTTGAAGATCAGCTG 3672
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Qy 3673 GAAAACATTCAGGTTCTCTAATCTCAATGAAAAGTGAAAATGGAAGGCACTAATTTCTCA 3732
Db 3721 GAAAACATTCAGGTTCTCTAATCTCAATGAAAAGTGAAAATGGAAGGCACTAATTTCTCA 3780
Qy 3733 CAACCAAACTCATTTGATTTTCTGCAAGCCAAAATGACCAACCTGCTAAAAAGAAAAG 3792
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Qy 3793 GGTTTATTTAATCCAGGAAAGAGACCTGCTTTAACCCACAGAGTTCTCTGCAATAC 3852
Db 3839 -----AGTTCTCTGCAATAC 3855
Qy 3853 AATGAGCTGAAGCTGGCCCTGGAAGAGGAAGCTGCTGTGAGAGTATGAGAGGCC 3912
Db 3856 AATGAGCTGAAGCTGGCCCTGGAAGAGGAAGCTGCTGTGAGAGTATGAGAGGCC 3915
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Db 3916 CTTCAAGAACCCGCAATGAGCTCCGCTCCGCGCGGAGAGAAAGTGCACCCGCAAGCA 3975
Qy 3973 ACGGACCAACCAACCCATCCACGCCACGCCACCGCGAGAGAGAGTCCCATATGTCGCC 4032
Db 3976 ACGGACCAACCAACCCATCCACGCCACGCCACCGCGAGAGAGAGTCCCATATGTCGCC 4035
Qy 4033 ATGCTGCGGTGCGCAGAGACACACGCCAGTGCATGAGCTGTGCGGCCCGCCATCCAGC 4092
Db 4036 ATGCTGCGGTGCGCAGAGACACACGCCAGTGCATGAGCTGTGCGGCCCGCCATCCAGC 4095
Qy 4093 CGCAGAAAGAGTCTTCAATCCAGAGAAATTTAGTGGCGTCTTAAAGAACATGACAC 4152
Db 4096 CGCAGAAAGAGTCTTCAATCCAGAGAAATTTAGTGGCGTCTTAAAGAACATGACAC 4155
Qy 4153 CACAATATTCCTCAACCGATTCACAGTAGAGCTGAACATGAGACCCCAAGTGTGCTG 4212
Db 4156 CACAATATTCCTCAACCGATTCACAGTAGAGCTGAACATGAGACCCCAAGTGTGCTG 4215
Qy 4213 TGTCTGATACCGTGCACTTTGAGACGCCAGACATCCAAATGTCTGCAATGTCAAGTGATG 4272
Db 4216 TGTCTGATACCGTGCACTTTGAGACGCCAGACATCCAAATGTCTGCAATGTCAAGTGATG 4275
Qy 4273 TGTCAACCCCAAGTGTCCCAAGTGTCTTCCAGCCACCTGCGGCTTGCTGTAATATGCC 4332
Db 4276 TGTCAACCCCAAGTGTCCCAAGTGTCTTCCAGCCACCTGCGGCTTGCTGTAATATGCC 4335
Qy 4333 ACAACATTCACCGAGGCTTCTGCGTGACCAAAATGAACCTCCCAAGTCTCCAGACCAAG 4392
Db 4336 ACAACATTCACCGAGGCTTCTGCGTGACCAAAATGAACCTCCCAAGTCTCCAGACCAAG 4395
Qy 4393 GAGCCACGACGACGCTTTCGACTGGAAGGGTGAAGAGTGTCCAGAAATACAAACGA 4452
Db 4396 GAGCCACGACGACGCTTTCGACTGGAAGGGTGAAGAGTGTCCAGAAATACAAACGA 4455
Qy 4453 GAGCAGCAAGGCTGGGACAGGAAGTCAATTTGCTGGAAGGATCAAAATCTCTCATTTAT 4512
Db 4456 GAGCAGCAAGGCTGGGACAGGAAGTCAATTTGCTGGAAGGATCAAAATCTCTCATTTAT 4515
Qy 4513 GACATGAAGCCAGAGAACCTGACAGAGCGCGTGAAGAAATTTGAGCTGTGCTTCCC 4572
Db 4516 GACATGAAGCCAGAGAACCTGACAGAGCGCGTGAAGAAATTTGAGCTGTGCTTCCC 4575
Qy 4573 GACGGGAGTATCTAATTTATGCTGCGTTTGTGCTTCCGAACCTGCAAAATACAGCCAA 4632
Db 4576 GACGGGAGTATCTAATTTATGCTGCGTTTGTGCTTCCGAACCTGCAAAATACAGCCAA 4635
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OY	4633	GC	-----	4635
Db	4636	GCA	ATGTCCTACATACATGAAGATGAATCTCACCCGACACACACTGCTGGCCCCGG	4635
OY	4636	-----	4635	
Db	4636	AGAAC	CCCTACTTGCTAGCTCCAGCTTCCCTGACAAACAGCCGCGGTACACGCCCTTA	4755
OY	4636	-----	4635	
OY	4636	-----	4635	
Db	4756	GAAT	CACTGTCGAGGTGGAGAGTTCTAGGAGAAAAAGAGAAAGCTGATGCTAAACTG	4815
OY	4663	CTTGG	AAACTCCCTGCTGAAACTGGAAAGTATGACCGTCTAGACATGAATCGACCGTG	4722
Db	4816	CTTGG	AAACTCCCTGCTGAAACTGGAAAGTATGACCGTCTAGACATGAATCGACCGTG	4875
OY	4723	CCCTT	CAGTACACAGGTGGTGGTGGGACCCGAGAAAGGGCTCTACGCCCTGAAATGTC	4782
Db	4876	CCCTT	CAGTACACAGGTGGTGGTGGGACCCGAGAAAGGGCTCTACGCCCTGAAATGTC	4935
OY	4783	TTG	AAAACTCCCTAACCATATGCTCCAGAAATGGAGACGCTTCCAAATTTATATTATC	4842
Db	4936	TTG	AAAACTCCCTAACCATATGCTCCAGAAATGGAGACGCTTCCAAATTTATATTATC	4995
OY	4843	AAGA	CTGAGAAAGCTACATGATAGCAGAGAAAGACGGGACATGTGTCTTGTGGAC	4902
Db	4996	AAGA	CTGAGAAAGCTACATGATAGCAGAGAAAGACGGGACATGTGTCTTGTGGAC	5055
OY	4903	GTG	AGAAAGTGGAAACAGTCCCTGGCCCAATGCCACTGCTGCCAGCCCGACATCTCA	4962
Db	5056	GTG	AGAAAGTGGAAACAGTCCCTGGCCCAATGCCACTGCTGCCAGCCCGACATCTCA	5115
OY	4963	CCCAA	CATTTTGAAGCTGCAAGGGCTGCACACTTGTGGGGAGGCAAGATTGAGAAC	5022
Db	5116	CCCAA	CATTTTGAAGCTGCAAGGGCTGCACACTTGTGGGGAGGCAAGATTGAGAAC	5175
OY	5023	GCG	CTGCACTGTGACAGCCATGCCCCAGCAAAAGTGTCTTCTCCGCTACACGAAAC	5082
Db	5176	GCG	CTGCACTGTGACAGCCATGCCCCAGCAAAAGTGTCTTCTCCGCTACACGAAAC	5235
OY	5083	CTG	AGCAATTCGTGATCGGAAAGATAGAGCTCAGAGCCCTGAGCTGTATCCAC	5142
Db	5236	CTG	AGCAATTCGTGATCGGAAAGATAGAGCTCAGAGCCCTGAGCTGTATCCAC	5295
OY	5143	TTCA	CCAAATTCAGTATCCTATTGGAAACCAATAAATTTCTAGAAATGACATGAGACG	5202
Db	5296	TTCA	CCAAATTCAGTATCCTATTGGAAACCAATAAATTTCTAGAAATGACATGAGACG	5355
OY	5203	TAC	AGCTGAGAAATTCCTGGATAGAAATGACATTCCTTGGACCTGCTGTGTTGGC	5262
Db	5356	TAC	AGCTGAGAAATTCCTGGATAGAAATGACATTCCTTGGACCTGCTGTGTTGGC	5415
OY	5263	GCG	CTTCCAAACAGTTCCCTGTCTCAATCGAGAGGTGAACAGGACAGGACAGAGAG	5322
Db	5416	GCG	CTTCCAAACAGTTCCCTGTCTCAATCGAGAGGTGAACAGGACAGGACAGAGAG	5475
OY	5323	GAG	TACTGTGTGTTTCACGAATTTGGAAGTTCGTGATTTCTTACGAAGAAGTAC	5382
Db	5476	GAG	TACTGTGTGTTTCACGAATTTGGAAGTTCGTGATTTCTTACGAAGAAGTAC	5535
OY	5383	CGC	ACAGATTCGAAGTGCCTTACCTTGGCTTGGCTACAGAAACCCAT	5442
Db	5536	CGC	ACAGATTCGAAGTGCCTTACCTTGGCTTGGCTACAGAAACCCAT	5595
OY	5443	CTG	TTTGACCACTTCAACTCACTCGAAGTATTTGATTCAGAGCACGCTCTCAACA	5502
Db	5596	CTG	TTTGACCACTTCAACTCACTCGAAGTATTTGATTCAGAGCACGCTCTCAACA	5655
OY	5503	GGA	ACCTCGCCAGGCTACTGGACATCCCGAACCCGCGCTACCTGGGCTCGCAT	5562
Db	5656	GGA	ACCTCGCCAGGCTACTGGACATCCCGAACCCGCGCTACCTGGGCTCGCAT	5715

Qy	5563	TCCTCAGAGCGATTACTTGGGGTCCCTCATDACCAGATAAATTAAAGGGTCATTGGCTGC	5622
Db	5716	TCCCTCAGAGCGATTACTTGGGGTCCCTCATDACCAGATAAATTAAAGGGTCATTGGCTGC	5775
Qy	5623	AAGGGAACCTCGTGAAGAGGTCCGCGACATGAAACCAACCGGGGGCCGCTCCACTCCCGC	5682
Db	5776	AAGGGAACCTCGTGAAGAGGTCCGCGACATGAAACCAACCGGGGGCCGCTCCACTCCCGC	5835
Qy	5683	AG 5684	
Db	5836	AG 5837	

RESULT 3
US-09-804-471A-1
; Sequence 1, Application US/09804471A

```

1 TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
2 TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
3 TITLE OF INVENTION: THEREOF
4 TITLE OF INVENTION:
5 FILE REFERENCE: CL001164
6 CURRENT APPLICATION NUMBER: US/09/804,471A
7 CURRENT FILING DATE: 2001-03-13
8 NUMBER OF SEQ ID NOS: 4
9 SOFTWARE: FastSeq for Windows Version 4.0
10 SEQ ID NO 1
11 LENGTH: 1515
12 TYPE: DNA
13 ORGANISM: Human
14 US-09-804-471A-1

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Query Match	22.6%	Score 1391.8;	DB 4;	Length 1515;
Best Local Similarity	99.5%;	Pred. No. 0;		
Matches 1396;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0;

QY	1	ATGTTGAAGTTCAAAATATNGAGCGCGGAATTCCTTTGATGCTGGTGTGCTGAACCCATT	60
Db	7	ATGTTGAAGTTCAAAATATNGAGCGCGGAATTCCTTTGATGCTGGTGTGCTGAACCCATT	66
QY	61	GCCAGCCGGGCTTCGAGGCTGAATCTGTTCTTCGAGGGGAAACCACTTTATGACTCA	120
Db	67	GCCAAACGGGCGTTCGAGGCTGAATCTGTTCTTCGAGGGGAAACCACTTTATGACTCA	126
QY	121	CAGAGATGTCCTCTCTTCCCGAAGGGATATTAGATGCCCTCTTGTTCTTTGAA	180
Db	127	CAGAGATGTCCTCTCTTCCCGAAGGGATATTAGATGCCCTCTTGTTCTTTGAA	186
QY	181	GAATGACATCAGCCTGCTCTGATGAATTAAGCAGCTGAGCAACTTTGTCCGAAATAT	240
Db	187	GAATGACATCAGCCTGCTCTGATGAATTAAGCAGCTGAGCAACTTTGTCCGAAATAT	246
QY	241	TCCGACACCAATAGTGAAGTTACAGGAGCTCCAGCTTCGGGAAAGGACTTCGAAGTGA	300
Db	247	TCCGACACCAATAGTGAAGTTACAGGAGCTCCAGCTTCGGGAAAGGACTTCGAAGTGA	306
QY	301	AGCTCTTGAGTTGTGTCACTTTGCTGAAGTGCAGGTGTTAAGAGAGAAAGCAACCGGG	360
Db	307	AGCTCTTGAGTTGTGTCACTTTGCTGAAGTGCAGGTGTTAAGAGAGAAAGCAACCGGG	366
QY	361	GACATCTATGCTAAGAAAGTGAATAAAGAGGCTTATTGGGCCGAGGACAGTTTCA	420
Db	367	GACATCTATGCTAAGAAAGTGAATAAAGAGGCTTATTGGGCCGAGGACAGTTTCA	426
QY	421	TTTTTTGAGGAGACCGGAACATTTATCTCGAAGCAAGACCCGTGATTCGCCCAATTA	480
Db	427	TTTTTTGAGGAGACCGGAACATTTATCTCGAAGCAAGACCCGTGATTCGCCCAATTA	486
QY	481	CAGATATGCTTTGAGCAAAATAACACCTTATCTGATGGAAGAAATTCAGGCTGAGGG	540
Db	487	CAGATATGCTTTGAGCAAAATAACACCTTATCTGATGGAAGAAATTCAGGCTGAGGG	546

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QY 541 GACTTGCTGTCACCTTTTGAATAGATAGAGACCACTAGATGAAAACTGATACAGTTT 600
| | | | |
Db 547 GACTTGCTGTCACCTTTTGAATAGATAGAGACCACTAGATGAAAACTGATACAGTTT 606
| | | | |
QY 601 TACCTAGCTGACGTGATTTTGGCTGTTACAGCGTTTCATGTAGGAGATACGTGATCGA 660
| | | | |
Db 607 TACCTAGCTGACGTGATTTTGGCTGTTACAGCGTTTCATGTAGGAGATACGTGATCGA 666
| | | | |
QY 661 GACATCAAGGCTGAGAACATTTCTGTTGACCGGACGAGACATCAAGCTGGTGGATTTT 720
| | | | |
Db 667 GACATCAAGGCTGAGAACATTTCTGTTGACCGGACGAGACATCAAGCTGGTGGATTTT 726
| | | | |
QY 721 GGAATCCGCGGAAAAATGAATTCAAACAAAGATGTGATGCCAAATCCCGATTTGGAGCC 780
| | | | |
Db 727 GGAATCCGCGGAAAAATGAATTCAAACAAAGATGTGATGCCAAATCCCGATTTGGAGCC 786
| | | | |
QY 781 CCAGATTAATGAGCTCTCTGAAGTGTGATCTGTATGAAAGGGAGTGGAAAAAGGCACTTAC 840
| | | | |
Db 787 CCAGATTAATGAGCTCTCTGAAGTGTGATCTGTATGAAAGGGAGTGGAAAAAGGCACTTAC 846
| | | | |
QY 841 GGCCTGGACTGTGACTGTGAGTCAAGTGGGCGTGAATTGCCATGAGATGATTTATGGGAGA 900
| | | | |
Db 847 GGCCTGGACTGTGACTGTGAGTCAAGTGGGCGTGAATTGCCATGAGATGATTTATGGGAGA 906
| | | | |
QY 901 TCCCCCTTGCGCAGAGGGAACTCTGCGCAGAACCTTCAATATGATTAATGATTTCCAGCGG 960
| | | | |
Db 907 TCCCCCTTGCGCAGAGGGAACTCTGCGCAGAACCTTCAATATGATTAATGATTTCCAGCGG 966
| | | | |
QY 961 TTTTGAATTTTCCAGATGATGACCCCAAGTGAAGAGAGATCTTTCTTGATCTGATTCAAAGC 1020
| | | | |
Db 967 TTTTGAATTTTCCAGATGATGACCCCAAGTGAAGAGAGATCTTTCTTGATCTGATTCAAAGC 1026
| | | | |
QY 1021 TTGTTGTGCGGCGCAGAAAGAGAGACTGAAGTTTGAAGGTCTTGTGCGCATCTTTCTTC 1080
| | | | |
Db 1027 TTGTTGTGCGGCGCAGAAAGAGAGACTGAAGTTTGAAGGTCTTGTGCGCATCTTTCTTC 1086
| | | | |
QY 1081 TCTAAATTTGATCTGGAACAACTTGTGAATCTCTCTCTCCCTGTTCCACCTCTCAAG 1140
| | | | |
Db 1087 TCTAAATTTGATCTGGAACAACTTGTGAATCTCTCTCTCCCTGTTCCACCTCTCAAG 1146
| | | | |
QY 1141 TCTGAGATGACACCTCCAAATTTTGAATGAAACGAGAAAGAAATTCGTGGGTTCATCTCT 1200
| | | | |
Db 1147 TCTGAGATGACACCTCCAAATTTTGAATGAAACGAGAAAGAAATTCGTGGGTTCATCTCT 1206
| | | | |
QY 1201 CCGTCCAGAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGTTTTCG 1260
| | | | |
Db 1207 CCGTCCAGAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGTTTTCG 1266
| | | | |
QY 1261 TACAGCAAGGCACTGGGGAATTTTGTGATGATCTGAGTCTGTGTGTGGGTCTGACTCC 1320
| | | | |
Db 1267 TACAGCAAGGCACTGGGGAATTTTGTGATGATCTGAGTCTGTGTGTGGGTCTGACTCC 1326
| | | | |
QY 1321 CCGTCCAGAGCTGAGCTCCATGAGAAAGAACTTCATCAATAAGAAAGAGTACAAAGC 1380
| | | | |
Db 1327 CCGTCCAGAGCTGAGCTCCATGAGAAAGAACTTCATCAATAAGAAAGAGTACAAAGC 1386
| | | | |
QY 1381 TCTCAGGACAAAGTCTCACAAGAT 1403
| | | | |
Db 1387 TCTCAGGACAAAGTCTCACAAGAT 1409
| | | | |
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RESULT 4
US-10-238-709-1

; Sequence 1, Application US/10238709
; Patent No. 6680188
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO01164DIV
; CURRENT APPLICATION NUMBER: US/10/238,709
; CURRENT FILING DATE: 2002-09-11

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NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1515  
; TYPE: DNA  
; ORGANISM: Human  
US-10-238-709-1  
  
Query Match 22.6%; Score 1391.8; DB 4; Length 1515;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1396; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
  
QY 1 ATGTTGAAGTTAAATATGAGCGCGGAATCCTTTGATGCTGCTGCTGAAACCCATT 60  
| | | | |  
Db 7 ATGTTGAAGTTCAATATATGAGCGCGGAATCCTTTGATGCTGCTGCTGAAACCCATT 66  
| | | | |  
QY 61 GCCAGCCGCGCTCCAGGCTGAATCTGTTCTTCCAGGGAAAAACCACTTTATGACTCA 120  
| | | | |  
Db 67 GCCAGCCGCGCTCCAGGCTGAATCTGTTCTTCCAGGGAAAAACCACTTTATGACTCA 126  
| | | | |  
QY 121 CAGCAGATGCTCTCTTTCCGAGAGAGGATATTAATGATGCTCTTGTCTTTGAA 180  
| | | | |  
Db 127 CAGCAGATGCTCTCTTTCCGAGAGAGGATATTAATGATGCTCTTGTCTTTGAA 186  
| | | | |  
QY 181 GAATGAGTCAAGCTGCTGATGAAAGATTAAGACGTAACCACTTGTCCGGAAGTAT 240  
| | | | |  
Db 187 GAATGAGTCAAGCTGCTGATGAAAGATTAAGACGTAACCACTTGTCCGGAAGTAT 246  
| | | | |  
QY 241 TCCGACACCATAGCTGATTAAGAGAGCTCCAGGCTTCCGAGAAAGACTTGAAGTCA 300  
| | | | |  
Db 247 TCCGACACCATAGCTGATTAAGAGAGCTCCAGGCTTCCGAGAAAGACTTGAAGTCA 306  
| | | | |  
QY 301 AGCTTTGAGTGTGTGCTCACTTTGCTGAAGTCAAGTGTGTAAGAGAAACCAACCGGG 360  
| | | | |  
Db 307 AGCTTTGAGTGTGTGCTCACTTTGCTGAAGTCAAGTGTGTAAGAGAAACCAACCGGG 366  
| | | | |  
QY 361 GACATCTATGCTATGAAGATGATGAAGAAAGGCTTTATTTGGCCCGAGGACAGTTTCA 420  
| | | | |  
Db 367 GACATCTATGCTATGAAGATGATGAAGAAAGGCTTTATTTGGCCCGAGGACAGTTTCA 426  
| | | | |  
QY 421 TTTTGTGAGAAAGCGGAACTATTAATCTGAAAGCAAGGCCGCTGATCCCAATTA 480  
| | | | |  
Db 427 TTTTGTGAGAAAGCGGAACTATTAATCTGAAAGCAAGGCCGCTGATCCCAATTA 486  
| | | | |  
QY 481 CAGATGCTCTTCAAGCAAAATACACCTTTATCTGATGAGAGAAATCACTGAGAGGG 540  
| | | | |  
Db 487 CAGATGCTCTTCAAGCAAAATACACCTTTATCTGATGAGAGAAATCACTGAGAGGG 546  
| | | | |  
QY 541 GACTTGCTGTCACTTTGAATAGATAGAGGACCAAGTTAGTGAACCTGATACAGTTT 600  
| | | | |  
Db 547 GACTTGCTGTCACTTTGAATAGATAGAGGACCAAGTTAGTGAACCTGATACAGTTT 606  
| | | | |  
QY 601 TACCTAGCTGACTGATTTTGGCTGTTACAGCGTTTCATGTAGGAGATACGTGATCGA 660  
| | | | |  
Db 607 TACCTAGCTGACTGATTTTGGCTGTTACAGCGTTTCATGTAGGAGATACGTGATCGA 666  
| | | | |  
QY 661 GACATCAAGGCTGAGAACTTCTGTTGACCGGACAGACACATCAAGCTGGTGGATTTT 720  
| | | | |  
Db 667 GACATCAAGGCTGAGAACTTCTGTTGACCGGACAGACACATCAAGCTGGTGGATTTT 726  
| | | | |  
QY 721 GGAATCCGCGGAAAAATGAATTCAAACAAAGATGTGATGCCAAATCCCGATTTGGAGCC 780  
| | | | |  
Db 727 GGAATCCGCGGAAAAATGAATTCAAACAAAGATGTGATGCCAAATCCCGATTTGGAGCC 786  
| | | | |  
QY 781 CCAGATTAATGAGCTCTCTGAAGTGTGATCTGTATGAAAGGGAGTGGAAAAAGGCACTTAC 840  
| | | | |  
Db 787 CCAGATTAATGAGCTCTCTGAAGTGTGATCTGTATGAAAGGGAGTGGAAAAAGGCACTTAC 846  
| | | | |  
QY 841 GGCCTGGACTGTGACTGTGAGTCAAGTGGGCGTGAATTGCCATGAGATGATTTATGGAGA 900  
| | | | |  
Db 847 GGCCTGGACTGTGACTGTGAGTCAAGTGGGCGTGAATTGCCATGAGATGATTTATGGAGA 906  
| | | | |  
QY 901 TCCCCCTTGCGCAGAGGGAACTCTGCGCAGAACCTTCAATATGATTAATGATTTCCAGCGG 960  
| | | | |
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Db	907	TCGCCCTTCGACAGGGAACTCTGCGCAGAACCTTCAATTAACTATTATATTTCCAGCGG	966
Qy	961	TTTTTGAATAATTCAGATGACCCCAAGATGACAGTGACTTTCTTGATCTGATTCAAAGC	1020
Db	967	TTTTTGAATAATTCAGATGACCCCAAGATGACAGTGACTTTCTTGATCTGATTCAAAGC	1026
Qy	1021	TTGCTTTCGCGGCACAAAAGAGAGACTGAAGTTTGAAGCTCTTTTGCTGCAATCCTTTCTTC	1080
Db	1027	TTGTTTTCGCGGCACAAAAGAGAGACTGAAGTTTGAAGGCTCTTTTGCTGCAATCCTTTCTTC	1086
Qy	1081	TCTAAATTTGACTGGAACAACATTCGTAACTCTCTCCGCCCTTCGTTCCGACCTCAAG	1140
Db	1087	TCTAAATTTGACTGGAACAACATTCGTAACTCTCTCCGCCCTTCGTTCCGACCTCAAG	1146
Qy	1141	TCTGACGATGACACCTCCAAATTTTGATGAACACAGAAAGAAATCGTGGGTTTCATCCTCT	1200
Db	1147	TCCGACGATGACACCTCCAAATTTTGATGAACACAGAAAGAAATCGTGGGTTTCATCCTCT	1206
Qy	1201	CCGTGCGCAGCTGAGCGCCCTCAGAGCTTCTCGGGTGAAAGACTCGCGTTTGTCGGGTTTTCG	1260
Db	1207	CCGTGCGCAGCTGAGCGCCCTCAGAGCTTCTCGGGTGAAAGACTCGCGTTTGTCGGGTTTTCG	1266
Qy	1261	TACAGCAAGGCACTGGGGATTTCTTGATGATCTGAGCTGTGTGTGTCGGGCTGAGACTCC	1330
Db	1267	TACAGCAAGGCACTGGGGATTTCTTGATGATCTGAGCTGTGTGTGTCGGGCTGAGACTCC	1336
Qy	1321	CTTGCAGAGACTAGCTCCATGAGAAAAGAACTTTCATCAAAAGCAAGAGCTACAAAGC	1380
Db	1327	CTTGCAGAGACTAGCTCCATGAGAAAAGAACTTTCATCAAAAGCAAGAGCTACAAAGC	1386
Qy	1381	TCTCAGCAGAGTGTCAACAAGT 1403	
Db	1387	TCTCAGCAGAGTGTCAACAAGT 1409	

RESULT 5
 US-09-774-528-419
 Sequence 419, Application US/09774528
 Patent No. 6743619
 GENERAL INFORMATION:
 APPLICANT: Tang, Y. Tom
 APPLICANT: Zhou, Ping
 APPLICANT: Goodrich, Kyle
 APPLICANT: Liu, Chengshua
 APPLICANT: Abundi, Vinod
 APPLICANT: Ren, Feiyang
 APPLICANT: Zhang, Jie
 APPLICANT: Zhao, Qing A.
 APPLICANT: Yang, Yonghong
 APPLICANT: Xue, Aildong J.
 APPLICANT: Wehrman, Tom
 APPLICANT: Wang, Jian-Rui
 APPLICANT: Wang, Dunrui
 APPLICANT: Dmanac, Radoje T.
 TITLE OF INVENTION: No. 6743619el Nucleic Acids and
 TITLE OF INVENTION: Polypeptides
 FILE REFERENCE: 802
 CURRENT APPLICATION NUMBER: US/09/774,528
 CURRENT FILING DATE: 2001-01-30
 NUMBER OF SEQ ID NOS: 441
 SOFTWARE: pt_FL_genes Version 2.0
 SEQ ID NO 419
 LENGTH: 2162
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (364)..(2010)
 US-09-774-528-419

Query Match	15.5%;	Score 952.4;	DB 4;	Length 2162;
Best Local Similarity	99.4%;	Pred. No. 3.9e-256;		

Matches 956; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY	1	ATGTTGAAGTTCAAAATATGAGCCCGGAATCTTTGAGTGTGCTGCTGAACCCATT	60
Db	364	ATGTTGAAGTTCAAAATATGAGCCCGGAATCTTTGAGTGTGCTGCTGAACCCATT	423
QY	61	GCGAGCGGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACACCCCTTATGACTCAA	120
Db	424	GCGAGCGGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACACCCCTTATGACTCAA	483
QY	121	CAGAGAGTGTCTCTCTTTTCCCGAAGGGATATTAGATGCCCTTTGTTCTCTTGA	180
Db	484	CAGAGAGTGTCTCTCTTTTCCCGAAGGGATATTAGATGCCCTTTGTTCTCTTGA	543
QY	181	GAATGCACTACGCTCTCTGTATGATTAAGCAGTGAACAACTTTGTCGGAAATAT	240
Db	544	GAATGCACTACGCTCTCTGTATGATTAAGCAGTGAACAACTTTGTCGGAAATAT	603
QY	241	TCCGACACATAGCTGAGTTACAGAGTCCAGGCTTCGGCAAAAGAACTTCGAAATCGA	300
Db	604	TCCGACACATAGCTGAGTTACAGAGTCCAGGCTTCGGCAAAAGAACTTCGAAATCGA	663
QY	301	AGCTCTGAGGTGTGCTCACTTTCGTAATGTCAGGTGTATAGAGAAAGCAACCGGG	360
Db	664	AGCTCTGAGGTGTGCTCACTTTCGTAATGTCAGGTGTATAGAGAAAGCAACCGGG	723
QY	361	GACATCTATGCTATGAAGATGATGAAGAAAGGCTTATTTGGCCGAGGACAGTTTCA	420
Db	724	GACATCTATGCTATGAAGATGATGAAGAAAGGCTTATTTGGCCGAGGACAGTTTCA	783
QY	421	TTTTTGAAGAAAGCGGAACATATTATCTGAAAGCAACGCGGTGATCCCAATTA	480
Db	784	TTTTTGAAGAAAGCGGAACATATTATCTGAAAGCAACGCGGTGATCCCAATTA	843
QY	481	CAGTATGCTTTCAAGCAAAAATCACCCTTATCTGATGAGAAATACGCTTGAAGG	540
Db	844	CAGTATGCTTTCAAGCAAAAATCACCCTTATCTGATGAGAAATACGCTTGAAGG	903
QY	541	GACTTGCTGTACATTTTGAATGATATGAGGACCAAGTTAGA TGA AAACTGATACAGTTT	600
Db	904	GACTTGCTGTACATTTTGAATGATATGAGGACCAAGTTAGTGA AAACTGATACAGTTT	963
QY	601	TACCTAGCTGAGTGAATTTTGGCTGTTCA CAGCCTTATCTGATGAGGATACGTGCATCGA	660
Db	964	TACCTAGCTGAGTGAATTTTGGCTGTTCA CAGCCTTATCTGATGAGGATACGTGCATCGA	1023
QY	661	GACATCAAAGCTTGAAACATTCTTGTTGACCGCACAGGACACATCAAAGCTGTGATTTT	720
Db	1024	GACATCAAAGCTTGAAACATTCTTGTTGACCGCACAGGACACATCAAAGCTGTGATTTT	1083
QY	721	GGATCTGCGGGA AAAATGAATTCAAACAAGATGGTAATGCGCAAACTCCGATTGGGAGC	780
Db	1084	GGATCTGCGGGA AAAATGAATTCAAACAAGATGGTAATGCGCAAACTCCGATTGGGAGC	1143
QY	781	CCAGATTAACATGAGCTCTGTAAGTGTCTGATCTGTATGAACGGGGATGGA AAAAGCACCTAC	840
Db	1144	CCAGATTAACATGAGCTCTGTAAGTGTCTGATCTGTATGAACGGGGATGGA AAAAGCACCTAC	1203
QY	841	GGCTCTGACTGTACTGTGTGCTAGTGGGGCTGATTTGCTATGAGATGATTTATGGGAGA	900
Db	1204	GGCTCTGACTGTACTGTGTGCTAGTGGGGCTGATTTGCTATGAGATGATTTATGGGAGA	1263
QY	901	TCGCCCTTGGCAGAGGGAACCTCTGCAGAACTTCAATATAACATTATGAATTTTCAGCGG	960
Db	1264	TCGCCCTTGGCAGAGGGAACCTCTGCAGAACTTCAATATAACATTATGAATTTTCAGCGG	1323
QY	961	TT 962	
Db	1324	TT 1325	

RESULT 6
US-09-916-204-1


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/ Sequence 1, Application US/09916204
/ Patent No. 6638745
/ GENERAL INFORMATION:
/ APPLICANT: WEI, Ming-Hui et al.
/ TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
/ TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
/ FILE REFERENCE: CLO01164CIP
/ CURRENT APPLICATION NUMBER: US/09/916,204
/ CURRENT FILING DATE: 2001-07-24
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 1133
/ TYPE: DNA
/ ORGANISM: Human
US-09-916-204-1

Query Match      12.2%; Score 750; DB 4; Length 1133;
Best Local Similarity 99.3%; Pred. No. 1.6e-199;
Matches 753; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGTGAAGTTCAAATATGAGAGCGGGAATCCTTGTGATGCTGTGCTGAACCCATT 60
DB 54 ATGTGAAGTTCAAATATGAGAGCGGGAATCCTTGTGATGCTGTGCTGAACCCATT 113
QY 61 GCCAGCGGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCAACCTTTATGACTCA 120
DB 114 GCCAGCGGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCAACCTTTATGACTCA 173
QY 121 CAGCAGATGTCCTCTCTTTCCGAGAAAGGATTAAGATGCCCTTTGTTCTTTGAA 180
DB 174 CAGCAGATGTCCTCTCTTTCCGAGAAAGGATTAAGATGCCCTTTGTTCTTTGAA 233
QY 181 GAATGAGTCAGGCTGCTCGATGAAGATTAAGCAAGTGAAGCACTTTTCCGGAAGTAT 240
DB 234 GAATGAGTCAGGCTGCTCGATGAAGATTAAGCAAGTGAAGCACTTTTCCGGAAGTAT 293
QY 241 TCCGACACCATATGAGTGAAGAGTCCAGGCTTCCGCAAGAGACTTCCGAAGTCA 300
DB 294 TCCGACACCATATGAGTGAAGAGTCCAGGCTTCCGCAAGAGACTTCCGAAGTCA 353
QY 301 AGCTTTGATGTTGTGTGTCTCTTGTGAAGTGCAGGTGTGAAGAGAAACCAACCGGG 360
DB 354 AGCTTTGATGTTGTGTGTCTCTTGTGAAGTGCAGGTGTGAAGAGAAACCAACCGGG 413
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DB 414 GACATCTATGCTATGAAGATGATGAAGAGAGGCTTTATTTGGCCGAGAGAGATTCA 473
QY 421 TTTTGTGAGAAAGCGGAAACATATTATCTCGAAGCAACAGCCCGTGTATCCCAATT 480
DB 474 TTTTGTGAGAAAGCGGAAACATATTATCTCGAAGCAACAGCCCGTGTATCCCAATT 533
QY 481 CAGTATGCTTTCAGGACAAATATCACTTTATCTGATGAGAGATATCAGCTTGAAGG 540
DB 534 CAGTATGCTTTCAGGACAAATATCACTTTATCTGATGAGAGATATCAGCTTGAAGG 593
QY 541 GACTTGCTGTCACTTTGATATGATATGAGACAGTATGATGAAGAAACCTGTACAGTT 600
DB 594 GACTTGCTGTCACTTTGATATGATATGAGACAGTATGATGAAGAAACCTGTACAGTT 653
QY 601 TACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGAGATACGTGCATGA 660
DB 654 TACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGAGATACGTGCATGA 713
QY 661 GACATCAAGCTGAGAAACATTTCTGTGACCGCAACAGACACATCAAGCTGTGATTTT 720
DB 714 GACATCAAGCTGAGAAACATTTCTGTGACCGCAACAGACACATCAAGCTGTGATTTT 773
QY 721 GGATCTGCCGCAAAATGAATTCAAACAAGATGTGAA 758
DB 774 GGATCTGCCGCAAAATGAATTCAAACAAGATGTGAA 811
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RESULT 7
US-10-282-048-1
/ Sequence 1, Application US/10282048
/ Patent No. 6692948
/ GENERAL INFORMATION:
/ APPLICANT: WEI, Ming-Hui et al.
/ TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
/ TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
/ FILE REFERENCE: CLO01164CIP-DIV
/ CURRENT APPLICATION NUMBER: US/10/282,048
/ CURRENT FILING DATE: 2002-10-29
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 1133
/ TYPE: DNA
/ ORGANISM: Human
US-10-282-048-1

Query Match      12.2%; Score 750; DB 4; Length 1133;
Best Local Similarity 99.3%; Pred. No. 1.6e-199;
Matches 753; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGTGAAGTTCAAATATGAGAGCGGGAATCCTTGTGATGCTGTGCTGAACCCATT 60
DB 54 ATGTGAAGTTCAAATATGAGAGCGGGAATCCTTGTGATGCTGTGCTGAACCCATT 113
QY 61 GCCAGCGGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCAACCTTTATGACTCA 120
DB 114 GCCAGCGGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCAACCTTTATGACTCA 173
QY 121 CAGCAGATGTCCTCTCTTTCCGAGAAAGGATTAAGATGCCCTTTGTTCTTTGAA 180
DB 174 CAGCAGATGTCCTCTCTTTCCGAGAAAGGATTAAGATGCCCTTTGTTCTTTGAA 233
QY 181 GAATGAGTCAGGCTGCTCGATGAAGATTAAGCAAGTGAAGCACTTTTCCGGAAGTAT 240
DB 234 GAATGAGTCAGGCTGCTCGATGAAGATTAAGCAAGTGAAGCACTTTTCCGGAAGTAT 293
QY 241 TCCGACACCATATGAGTGAAGAGTCCAGGCTTCCGCAAGAGACTTCCGAAGTCA 300
DB 294 TCCGACACCATATGAGTGAAGAGTCCAGGCTTCCGCAAGAGACTTCCGAAGTCA 353
QY 301 AGCTTTGATGTTGTGTGTCTCTTGTGAAGTGCAGGTGTGAAGAGAAACCAACCGGG 360
DB 354 AGCTTTGATGTTGTGTGTCTCTTGTGAAGTGCAGGTGTGAAGAGAAACCAACCGGG 413
QY 361 GACATCTATGCTATGAAGATGATGAAGAGAGGCTTTATTTGGCCGAGAGAGATTCA 420
DB 414 GACATCTATGCTATGAAGATGATGAAGAGAGGCTTTATTTGGCCGAGAGAGATTCA 473
QY 421 TTTTGTGAGAAAGCGGAAACATATTATCTCGAAGCAACAGCCCGTGTATCCCAATT 480
DB 474 TTTTGTGAGAAAGCGGAAACATATTATCTCGAAGCAACAGCCCGTGTATCCCAATT 533
QY 481 CAGTATGCTTTCAGGACAAATATCACTTTATCTGATGAGAGATATCAGCTTGAAGG 540
DB 534 CAGTATGCTTTCAGGACAAATATCACTTTATCTGATGAGAGATATCAGCTTGAAGG 593
QY 541 GACTTGCTGTCACTTTGATATGATATGAGACAGTATGATGAAGAAACCTGTACAGTT 600
DB 594 GACTTGCTGTCACTTTGATATGATATGAGACAGTATGATGAAGAAACCTGTACAGTT 653
QY 601 TACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGAGATACGTGCATGA 660
DB 654 TACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGAGATACGTGCATGA 713
QY 661 GACATCAAGCTGAGAAACATTTCTGTGACCGCAACAGACACATCAAGCTGTGATTTT 720
DB 714 GACATCAAGCTGAGAAACATTTCTGTGACCGCAACAGACACATCAAGCTGTGATTTT 773
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Qy 752 TGGTGAATCCAACTCCGATTTGGAGCCCGAGATTACATGGCTCCTGAAGTGTGACTG 811
Db 1621 CGGTTCAGTCCCTCAGTGGCTGTAGGAATCCAGATTATATCTCTCTGAAATCTTTCAAG 1680
Qy 812 TGATGAACGGGGATGGAAAAAGGACCTAGGGCCCTGGAGCTGTGACGTGTGACGTGGGG 871
Db 1681 CCAATGAG--ATGGAAGAGGAGATATGACCTGATATGATGCTGTGTCTTTGGGGG 1737
Qy 872 TGATGGCTATGAGATTTATGAGAGATCCCTCTTCAGAGGAACTCTGCCAGAA 931
Db 1738 TCTGTATGATGAATATGCTTTACGGAGAAACCATTTATGAGAAATGCTGTGTGAGA 1797
Qy 932 CCTTCATATACATTATGAATTTCCAGCGGTTTGAATTTCCAG--ATGACCCCAAG 988
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Qy 989 TGAGCAGTACTTTCTGTATCTGATTCAGAGCTGTGTGGCGCCAGAAAGAGAGACT-- 1046
Db 1858 TGTCTGAAAAATGCTAAGAGATCTTATTCGAAGGCTCATTTGTAGCAGAGAACATCGACTTG 1917
Qy 1047 -----GAAGTTGAAGGCTTTTCTGCTCCATCTTTCTCTTAATTTGACTGGAGA 1099
Db 1918 GTCAAAATGGAATGAAAGACTTTAAGAAACACCATTTTCACTGGAATTTGATGGAGA 1977
Qy 1100 ACATTGTACTCTCTCCCTCCCTGTTCCACCTCAAGTCTGACATGACACTTCA 1159
Db 1978 AATATTCGAATCTGTGAAGCACTTATATTCAGAACTGTAGAGCCCAAGATACATCGA 2037
Qy 1160 ATTTGATGAACAGAGAAAGAAATGCGGGTTTCATCCCTCCGTCGACGAGCCGCT 1219
Db 2038 ATTTGATGATGATGATGATGATTTTAAAAAATTTGAAACGATGCCCAACACATCA 2097
Qy 1220 CAGGCTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCATCA 1264
Db 2098 CTGCATTTTCTGGCCACCACTGCGCATTTGTTGTTTACATATA 2142

RESULT 10
US-08-422-699A-12
; Sequence 12, Application US/08422699A
; Patent No. 5955265
; GENERAL INFORMATION:
; APPLICANT: Brook, J. David
; APPLICANT: Housman, David E.
; APPLICANT: Shaw, Duncan J.
; APPLICANT: Harley, Helen G.
; APPLICANT: Johnson, Keith J.
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
; DYSTROPHY GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02713
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,699A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/422,706
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/023,612

; FILING DATE: 26-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/839,255
; FILING DATE: 20-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/01545
; FILING DATE: 19-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00253
; FILING DATE: 05-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB9202485.0
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-5830A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2726 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-422-699A-12
Query Match 3.6%; Score 220.8; DB 2; Length 2726;
Best Local Similarity 53.7%; Pred. No. 1.1e-50;
Matches 531; Conservative 0; Mismatches 442; Indels 15; Gaps 3;
Qy 194 CTGCTGTGATGAAGTTTAAGCAGTGTGACACTTTGTCCGAAATTTCCAGACACCATAG 253
Db 243 CGAACTGGCCCGAGACAAAGTACGTGGCCGACTTCTTCAAGTGGCGGAGGCCATCGGG 302
Qy 254 CTGAATTCAGAGGCTTCAGAGCTTGGGCAAGGACTTGGAAAGTCAAGATCTTGAAGTT 313
Db 303 TGAGCTTAAGAGAGGTCCGACTGTCAGAGAGGACGACTTTCGAAATTTGAAAGTATCGAC 362
Qy 314 GTGTCTACTTTGCTGATGATGAGGAGTGTGAAGAGAAAGCAACCGGGAGCATCTATGTCTA 373
Db 363 GCGGGGCGCTTACGAGAGTGAAGGAGTGAAGATGAAGCAAGCGGGCCAGGTGTATGCCA 422
Qy 374 TGAAGTGTGAAGAAAGGCTTTATGGCCAGAGACAGGTTTCAATTTTGAAGAG 433
Db 423 TGAAGATCATGAACAGTGGGACATGCTGAAGAGGGGAGAGGTGTCGTGCTTCGCTGAGG 482
Qy 434 AGCGAACAATATCTGGAAGCAACAGCCCGTGGATCCCCCAATTACAGTATGCTTTC 493
Db 483 AGAGGAGCTGTGGTGAATGGGACCGGCGGTGATACGACGCTGACCTTCGCTTCC 542
Qy 494 AGGCAAAAATCACTTTATCTGATGAGAGAAATATCAGCTGGAGGGGACTTGTCTGAC 553
Db 543 AGGATGAGAACTACTGTAACGTGTGATGAGTATTAAGTGGCGGGGACCTGTGACAC 602
Qy 554 TTTTGAATGATATGAGAGCAAGTATGATGAAGAAACCTGATACAGTTTATACCTGATGAC 613
Db 603 TGCTGAGCAAGTTTGGGAGGCGGATTCGCGCGAATGAGCGGCTTCACTGCGGGAGAG 662
Qy 614 TGATTTTGGCTGTTCACAGCGTTTCACTGATGAGGATAGTGTGATGAGACATCAAGCTG 673
Db 663 TTGTATGCGCATATGACTGCGGTGACCGGCTTGGCTTACGTGACAGGAGCATCAAAACCG 722
Qy 674 AGAATTTCTGTTGACCGCAGAGACACATCAAGCTGTGATTTTGAATCTGCGCGGA 733
Db 723 ACAATCTCTGTGAGCCGCTGTGGCCATCTCCGCTGCGGAGACTTTCGCTTTCCTCA 782
Qy 734 AATGAATTCAAACAGATGTGAATGCCAAATCTCCGATTTGGAGCCCGCAATTCATAG 793
Db 783 AGCTCGGGCAGATGAACGCTGCGGTGCTGTGTGGCTGTGGGCCCCCAAGCTACCTGT 842
Qy 794 CTCCTGAAGTGTGA---CTGTGATGAACGGGGATGAAAAAGGACCTAAGGCTGAGCT 850

Db 843 CCCCCGATCTCGACGCTGTGGCGGTGGCGGAGCAGGAGCTACGGGCGGAGT 902
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Db 903 GTGACTGTGTGTGAGCGGTGTGTATTCCTATGATGATGATTTGAGAGATCCCGCTTCG 962
Qy 911 CAGAGGAACTCTGCGCAGAACCTTCAATTAATGATTTCCAGCGGTTTGTGAAT 970
Db 963 ACACGATTTCCAGCGCGGAGACCTATGCGAATGCTCCACTCAGAGACACCTCTCTC 1022
Qy 971 TTCAGATGACCCCAAGTGAAGT---GACTTCTTGTGATGATTTCAAGCTTTGTT 1027
Db 1023 TGCGGCTGTGAGAGAGGAGTCCCTGAGAGGCTGAGACTTCACTTCAAGGTTGCTGT 1082
Qy 1028 GCGGCCAGAAAGAGAGCTGAAGTTGAAGCTTTGCTC-----CATCTTCTT 1078
Db 1083 GTCCCCCGAGACAGCGCTGGCGGAGTGAAGCAGGCACTTCCGACACATCCCTTCT 1142
Qy 1079 TCTCTAAATTTGACTGAGACATTTGTATCTCTCCCGCTTGTCCACCTCA 1138
Db 1143 TCTTGGCTGTGACTGGATGTCTCCGAGACAGCGTCCCTTTACACCGGATTTG 1202
Qy 1139 AGTGTGACGATGACACCTCCCAATTTGA 1166
Db 1203 AAGGTCCACCGACACATGCACTTGA 1230

RESULT 11
US-08-422-7068-12
Sequence 12, Application US/08422706B
Patent No. 5977333
GENERAL INFORMATION:
APPLICANT: Brook, J. David
APPLICANT: Housman, David E.
APPLICANT: Shaw, Duncan J.
APPLICANT: Harley, Helen G.
APPLICANT: Johnson, Keith J.
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02713
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,706B
FILING DATE: 14-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/284,543
FILING DATE: 08-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612
FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/839,255
FILING DATE: 20-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB9202485.0
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5830A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2726 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-422-7068-12
Query Match 3.6%; Score 220.8; DB 2; Length 2726;
Best Local Similarity 53.7%; Pred. No. 1.1e-50;
Matches 531; Conservative 0; Mismatches 442; Indels 15; Gaps 3;
Qy 194 CTGCTGTATGAAATTAAGACGTGAGCACTTGTCCGAAATTCGACACCATAG 253
Db 243 CCGAATGCGCCAGGACAGTACGTGCGCACTTCTTGACGTGGCGGAGCCATGCTG 302
Qy 254 CTGAGTTACAGAGCTCCAGCCTTGGCGAAAGACTTGCAGACTCTTGTAGCTT 313
Db 303 TGAGCTTAAGAGAGTCCAGTGCAGAGGAGACCTTGAATTCGAGGTGATCGAGC 362
Qy 314 GTGCTCACTTGTCTGAGAGTGCAGGTGTGAAGAGAAAGCAACCGGAGCATCTATGCTA 373
Db 363 GCGGGCGCTTACAGCAGAGTACGTGATGTAATGAAGACAGACGCGCCAGGTATGCCA 422
Qy 374 TGAAGTATGAAAGAAAGGCTTTATTTGCGCCAGAGAGCGTTTCATTTTGAAGAG 433
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Qy 494 AGGACAAATATACCTTTATCTGATGAGAGATATCAGCGCTGAGGAGACTTGTCTAC 553
Db 543 AGGATGAGAACTACCTGTACCTGTGATGATGATATTAAGTGGCGGAGACTGTGACAC 602
Qy 554 TTTTGAATGATATGAGACCAAGTATGATGAAACCTGATATACGTTTACCTAGTAGC 613
Db 603 TGTGAGCAAGTTTGGGAGCGGATTCGCGCGAGATGGCGGCTTCTACCTGGCGAGA 662
Qy 614 TGATTTGGCTGTTCACAGCTTCATCTGATGGGATACGTGATGAGACATCAACCTTG 673
Db 663 TTGTCAATGACATGACCTGTGACACCGCTTGGCTGACCTGACAGGACATCAACCCG 722
Qy 674 AGAACATTTCTGTTGACCGCAGAGACATCAAGGTGTGATTTTGGATCTGCGCGCA 733
Db 723 ACAACATCTGTGACCGCTGTGACACATCCGCTGCGCACTTGGCTTGTGCTCA 782
Qy 734 AATGAAATCAACAAGATGATGAAATGCCAACTCCGATTGGGACCCCGAATTAATG 793
Db 783 AGCTGGGCGCATGAGAGAGTGGCGGTGCTGTGTGCTGTGGACCCCAAGCTACCTGT 842
Qy 794 CTCCTGAAGTCTGA---CTGTGATGAGAGGAGATGAGAAAGGACCTACGCGCTGAGCT 850
Db 843 CCCCCGATCTCGACGCTGTGGCGGTGGCGGAGCAGGAGCTACGGGCGGAGT 902
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Db 903 GTGACTGTGTGTGAGCGGTGTGTATTCCTATGATGATGATTTGAGAGATCCCGCTTCG 962
Qy 911 CAGAGGAACTCTGCGCAGAACCTTCAATTAATGATTTCCAGCGGTTTGTGAAT 970
Db 963 ACACGATTTCCAGCGCGGAGACCTATGCGAATGCTCCACTCAGAGACACCTCTCTC 1022

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OY 1079 TCTCTAAATTTGACTGTGAACAACATTCGTAATCTCTCTCCCTTGTGTTTCCACCTCA 1138
Db 1143 TCTTTGGCTGACTGAGATGGTCTCCGGGACAGCGTGCCTCCCTTTACACCGGATTTTG 1202
OY 1139 AGCTGACGATGACACCTTCATTTTGA 1166
Db 1203 AAGTGCCACCGACACATGCAACTTCGA 1230

RESULT 12
US-08-422-699A-8
; Sequence 8, Application US/0842269A
; Patent No. 5955265
; GENERAL INFORMATION:
; APPLICANT: Brook, J. David
; APPLICANT: Housman, David E.
; APPLICANT: Shaw, Duncan J.
; APPLICANT: Harley, Helen G.
; APPLICANT: Johnson, Keith J.
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
; TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Miltia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02713

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,699A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/422,706
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612
FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/839,255
FILING DATE: 20-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB9202485.0
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5830A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

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	LENGTH: 2511 base pairs	
1	TYPE: nucleic acid	
2	STRANDEDNESS: double	
3	TOPOLOGY: linear	
4	MOLECULE TYPE: DNA (genomic)	
5	FEATURE:	
6	NAME/KEY: CDS	
7	LOCATION: 1..1746	
8	US-08-422-699A-8	
Query Match	3.5%; Score 214; DB 2; Length 2511;	
Best Local Similarity	54.2%; Pred. No. 8,6e-49;	
Matches 508; Conservative	0; Mismatches 415; Indels 15; Gaps 3	
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QY	304 CTTTGAAGTTGTGTCACCTTGTCTGAAGTCAGAGTGTGAAGAGAAACCAACCGGGGAC 363	
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QY	364 ATCTATGCGATGAAGAATGTAAGAAAGAGCGCTTATTTGGCCAGAGACGAGTTTCAATT 423	
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QY	424 TTGAGAGAGACGGAAACATATTTATCTCGAAGACACAAGCCCTGTGATCCCCCAATTACAG 483	
DB	223 TTCGCTGAGAGAGAGGACGCTGTGTGAATGGGAGCCGGCGGTGATACGACAGCTGCAC 282	
QY	484 TATGCGCTTTCAGGACAAAATCACTTTATCTGATGAGAGAAATATCAGCTGGAAGGGAC 543	
DB	283 TTGCGCTTTCAGAGAGAGAACTACCTGTACCTGTGATGAGATATTAACGTGGCGGGGAC 342	
QY	544 TTGCTGTCACTTTGAATAGATATAGAGACCAAGTAGATGAAGAAACCTGATCAGTTTAC 603	
DB	343 CTGCTGACACTGCTGACGAGAGTTTGGGAGCGGATTTCCGCGCAGATGGCGCTTCTAC 402	
QY	604 CTAGCTGAGCTGATTTGGCTGTTCACAGCGTTCACTGATGGAGTACGTCATCGAGAC 663	
DB	403 CTGGGGGAGATTTGTCATGCGCAATAGACTCGGTGCACCGGCTTGGCTACGTCACAGGGAC 462	
QY	664 ATCAAGCCCTGAGGAACATTCTGTGTTGACCGGACAGGACATCAACACTGCTGATTTTGA 723	
DB	463 ATCAACCCGACACATCTCTGTGAGCCGCTGTGGCAATCCGCTTGGCCGACATTCGCG 522	
QY	724 TCTGCCGGAAATGAATTCAACAGAGTGTGATGCAAACTCCGATTTGGAGCCCCA 783	
DB	523 TCTTGCTCAAGCTGCGGGCAGATGGAACGGTGCGGTGCTGTGTGGCTGTGGGACCCCA 582	
QY	784 GATTACATGGCTCCTCGA--AGTGTGACTGTGATGAACGGGGATGAAAAAGCACCTTAC 840	
DB	583 GACTACCTGTCCCCCGAATCTCTGACGCTGTGGCGGTGGGCGCTGGGACAGCGACGTAC 642	
QY	841 GAGCTGACTGTGACTGTGTGCTCAAGTGGGCTGTGATTTGCTTATGAGATTTATTTAGGAGA 900	
DB	643 GGGGCCGAGTGTGACTGTGTGGCCCTGGGTGTATTCCGCTATGAATTTTCTAATGGCAG 702	
QY	901 TCCCCCTTGCAGAGGGAACCTCTGCCAAGACTTCAATTAATTATGAATTTCCAGCGG 960	
DB	703 ACGCCCTTCTTAAGGGGATTTCCACGCGCGGAGACTTATGGCAAGATCGTCCATCAAGAGAG 762	
QY	961 TTTTGAATAATTCAGATGACCCCAAGTGGCAGT---GACTTCTTGAATCTGATTTCA 1017	
DB	763 CACCTCTCTCTGCGCGCTGTGTGAGAGAAAGGGTCCCTGAGAGGCGCTCGAGACTTCAATTCAG 822	
QY	1018 AGCTTGTGTGCGGCGCAAGAAAGAGACGTGAAGTTTGAAGGTCTTTGTGTC----- 1068	
DB	823 CGTTTGTCTGTGTCCCGGAGACACGCGCTGGGCGGGGTTGAGACAGGGAATTCCGAGCA 882	
QY	1069 CATCTCTTCTTCTTAATAATTGACTGGAACAACATTTGTATCTTCTCTCCCTCTTGCTT 1128	
DB	883 CATCTCTTCTTCTTGTGCTGACTGTGAATGTGTCTGGGACACGCGTCCCTCTTTTACA 942	

QY 1129 CCCACCTCAAGTCTGACGATGACACTTCCATTGGA 1166
DB 943 CCGGATTCGAAGTGCCACCGACATGCACTTGA 980

RESULT 13

US-08-422-706B-8
Sequence 8, Application US/08422706B

Patent No. 5977333

GENERAL INFORMATION:

APPLICANT: Brook, J. David

APPLICANT: Housman, David E.

APPLICANT: Shaw, Duncan J.

APPLICANT: Harley, Helen J.

APPLICANT: Johnson, Kelch J.

TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC

TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Millita Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: US

ZIP: 02713

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/422,706B

FILING DATE: 14-APR-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/284,543

FILING DATE: 08-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/023,612

FILING DATE: 26-FEB-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/839,255

FILING DATE: 20-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/01545

FILING DATE: 19-FEB-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB93/00253

FILING DATE: 05-FEB-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB9202485.0

FILING DATE: 06-FEB-1992

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: MIT-5830A2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 2511 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1746

US-08-422-706B-8

Query Match

3.5% Score 214; DB 2; Length 2511;

Best Local Similarity 54.2%; Pred. No. 8.6e-49;
Matches 508; Conservative 0; Mismatches 415; Indels 15; Gaps 3;

QY 244 GACACCATAGCTGAGTTACAGAGCTCCAGCTTGGCAAAGACTTCCAGATCAGAACT 303
DB 43 GCCATGCTGTAGAGCTTAAGGAGGTCCGACTGACAGAGAGAGACTTCCAGATTCGAAG 102
QY 304 CTGTAGTGTGTGTGCTTGTGCTGAGTGCAGGTGTGTAAGAGAGAAACCAACCGGGGAC 363
DB 103 GTGATGAGAGCGGGGCGTTGACAGGAGTAGCGGTGTAAGATGAAAGACAGAGCGGAC 162
QY 364 ATCTATGCTATGAAAGTGTGTAAGAGAGAGGCTTTATTTGGCCAGAGAGGTTTCATTT 423
DB 163 GTGTATGCTATGAAAGTGTGTAAGAGAGAGGCTTTATTTGGCCAGAGAGGTTTCATTT 222
QY 424 TTGAG 483
DB 223 TTCGGTAG 282
QY 484 TATGCTTTCAG 543
DB 283 TTGCTTTCAG 342
QY 544 TTGCTTTCAG 603
DB 343 CTGCTTTCAG 402
QY 604 CTAGTGTGCTTTCAG 663
DB 403 CTGCTTTCAG 462
QY 664 ATCAAGCTGAG 723
DB 463 ATCAAGCTGAG 522
QY 724 TCTGCTTTCAG 783
DB 523 TCTGCTTTCAG 582
QY 784 GATTACATGAGCTTCTGA---AGTGTGCTGATGATGAGAGAGAGAGAGAGAGAGAGAG 840
DB 583 GACTTACCTGCTTCTGA---AGTGTGCTGATGATGAGAGAGAGAGAGAGAGAGAGAG 642
QY 841 GGGCTGAG 900
DB 643 GGGCTGAG 702
QY 901 TCCCTTTCAG 960
DB 703 AGCTTTCAG 762
QY 961 TTTTGAATTCAG 1017
DB 763 CACCTTTCAG 822
QY 1018 AGCTTTCAG 1068
DB 823 CCGTTCAG 882
QY 1069 CATCTTTCAG 1128
DB 883 CATCTTTCAG 942
QY 1129 CCCACCTCAAGTCTGACGATGACACTTCCATTGGA 1166
DB 943 CCGGATTCGAAGTGCCACCGACATGCACTTGA 980

RESULT 14
US-08-484-044-11
Sequence 11, Application US/08484044
Patent No. 5552282
GENERAL INFORMATION:

```

/ APPLICANT: Caskey, C. T.
/ APPLICANT: Fu, Ying-Hui
/ APPLICANT: Friedman, David L.
/ APPLICANT: Pizzuti, Antonio
/ APPLICANT: Fenwick, Raymond G.
/ TITLE OF INVENTION: Diagnosis of Myotonic Muscular Dystrophy
/ NUMBER OF SEQUENCES: 13
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fulbright & Jaworski, L.L.P.
/ STREET: 1301 McKinney, Suite 5100
/ CITY: Houston
/ STATE: Texas
/ COUNTRY: U.S.A.
/ ZIP: 77010-3095
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/484,044
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/019,940
/ FILING DATE: 19-FEB-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Paul, Thomas D.
/ REGISTRATION NUMBER: 32,714
/ REFERENCE/DOCKET NUMBER: D-5443
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 713/651-5325
/ TELEFAX: 713/651-5246
/ TELEX: 762829
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3182 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-08-484-044-11

Query Match      3.5%; Score 213.6; DB 1; Length 3182;
Best Local Similarity 54.2%; Pred. No. 1.3e-48;
Matches 507; Conservative 0; Mismatches 414; Indels 15; Gaps 3;

QY 246 CACCATAGCTAGTACAGAGAGCTCCAGCTTCGGCAAGAGCTTGAAGTCAAGATCT 305
DB 743 CATCTGTGAGAGCTTAAGAGAGCTCCGACTGCAGAGGAGCACTTCGAGATTCTGAAGT 802
QY 306 TGTAGGTTGTGTCATTTGCTGAAGTGCAGGTGTTAAGAGAGCAACCGGGAGACT 365
DB 803 GATCGAGCGGGGGGTTGAGGAGGTAGCGGTAGTGAAGTGAAGCAAGCGGCGAGGT 862
QY 366 CATGCTATGAAGAAGTGAAGAAGAGGCTTTATTGCGCCAGAGAGGTTTCAATTTT 425
DB 863 GTATCCCATGAAGATCATGAACAGTGGGACATGCTGAAGAGGGCGAGGTGCTGCTT 922
QY 426 TGAGGAAGAGCGGAACATATTATCTCGAAGCAAGCCCGGTGATCCCAATTACAGTA 485
DB 923 CCGTAGAGAGAGGAGCGTGTGTGTAATGGGAGCCGGGGTGAATCAAGCAAGCTGCACTT 982
QY 486 TGCCTTTAGAGCAAAAAATCACTTTATCTGATGAGAGATATCAAGCTGAGGGGAGCTT 545
DB 983 CGCCTTCCAGATGAGAACTACCTGTACCTGTATGAGATATTAAGTGGGCGGAGACT 1042
QY 546 GCTGCACTTTTGAATATATATAGAGACCAAGTTAGATAAAACTGATACAGTTTACTT 605
DB 1043 GCTGCACTGTGAGCAAGTTTGGGAGCGGATTCGGGCGGAGATGGCGGCTTCACT 1102
QY 606 AGCTGAGCTGATTTTGGCTGTTCACAGGCTTCATCTGATGGGATACGTCATCGAGCAT 665

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DB 1103 GGCGAGATTTTCATAGCCCATAGACTCGGTGACCGGCTTGGCTACGTGCACAGGACAT 1162
QY 666 CAAGCTGAGAACATTTCTGTTGACCGACAGAGACATCAAGCTGTGGATTTTGGATC 725
DB 1163 CAATCCGACAAATCTCTGCTGACCGCTGTGGCCATCTCGCTGGCCGACTTGGGCTC 1222
QY 726 TGGCGGAAAATGAATTCAAACAAGATGTGAATCCAAACTCCGATTTGGAGCCCA 785
DB 1223 TTGCTCAAGCTGCGCGGAGATGGAACGGTGGCTGTGCTGTGTGGGACCCCA 1282
QY 786 TTACATGAGCTCTGA---AGTGTGATGTATGAACGGGAGATGGAATAAGCACTAGG 842
DB 1283 CTACCTGTCCCGAGATCTGACAGCTGTGTGGCGGTGGCTGGAGACAGGAGCTAGCG 1342
QY 843 CCTGGAAGTGTGACTGTGTGTGATGAGTGGCGGTGATTTGCTATGATATTTAGAGATC 902
DB 1343 GCCGAGTGTGACTGTGTGTGGGCGGTGGTGTATTTGCTATGAATTTTATGGCAAC 1402
QY 903 CCCCTTCCAGAGGAGAACTCTGCCAACAACCTTCAATATCAATTAATTTCCAGCGGT 962
DB 1403 GCCCTTCAAGCGGATTCACAGCGCGAGACCTATGGCAAGTGTCCACTACAAAGAGCA 1462
QY 963 TTTGAATTTTCCAGATGACCCCAAGTGAAGT---GACTTCTGATCTGATTCGAAG 1019
DB 1463 CCTCTCTGTGCGCTGTGTGAGAGAGGCTCTGAGAGAGGCTGAGACTTCAATTCACGG 1522
QY 1020 CTTGTTGTGCGGCGCAAGAAAGAGACTGAAGTTGAAGTCTTGTCTGEC-----CA 1070
DB 1523 GTTGCTGTGTCGCCCGAGAGACAGGCTGGCGGGGTGGACAGAGCGACTTCGGAGACCA 1582
QY 1071 TCCCTTCTCTCTAAATTTGATCTGGAACAACATTCGTACTCTCTCCCTTCTGTTCC 1130
DB 1583 TCCCTTCTCTTGTGGCCCTGACTGAGTGGATGTCTCCGGAGACGCTGCCCTTTACACC 1642
QY 1131 CACCCTCAAGTCTGACATGACACCTCCATTTTGA 1166
DB 1643 GGATTTGCAAGTGCACCGACATGCACTTGA 1678

RESULT 15
US-09-804-471A-3
/ Sequence 3, Application US/09804471A
/ Patent No. 6479269
/ GENERAL INFORMATION:
/ APPLICANT: WEBSTER, Marion et al
/ TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
/ TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
/ FILE REFERENCE: CL001164
/ CURRENT APPLICATION NUMBER: US/09/804,471A
/ CURRENT FILING DATE: 2001-03-13
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 3
/ LENGTH: 174493
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(174493)
/ OTHER INFORMATION: n = A,T,C or G
US-09-804-471A-3

Query Match      3.3%; Score 205; DB 4; Length 174493;
Best Local Similarity 100.0%; Pred. No. 6.5e-45;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 753 GGTGAATGCCAAACTCCGATTTGGAGCCCGAGATTAATGAGCTCCGAAATGCTGACTGT 812
DB 130289 GGTGAATGCCAAACTCCGATTTGGAGCCCGAGATTAATGAGCTCCGAAATGCTGACTGT 130348
QY 813 GATGAACGGGGATGAGAAAAGCACTTACGAGCTGAGCTGTGACTGTGTGCTAGTGGGCGT 872

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Db      130349 GATGAACGGGGATGGAAGCACTACGGCTGACTGTGACTGGTCAGTGGCGT 130408
Qy      873  |||||GCTATGAGATGATTTATGGGATCCCCCTTCGAGAGGGAACCTTGGCCGAAAC 932
Db      130409 GATGGCTATGAGATGATTTATGGGATCCCCCTTCGAGAGGGAACCTTGGCCGAAAC 130468
Qy      933  CTTCAATAACATTATGAAATTTCCAG 957
Db      130469 CTTCAATAACATTATGAAATTTCCAG 130493

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Search completed: March 2, 2005, 17:05:19
 Job time : 902.401 secs

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